

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2004, 18:31:42 ; Search time 61.6875 Seconds

Perfect score: 262  
Sequence: 1 MEQAPEDQGPOREPYNEWTL.....SEAVRHFPRIWLHNNGQHIV 47  
273.318 Million cell updates/sec

Title: US-09-913-927D-2  
Scoring table: BIOSUM62  
Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_GenSeq\_23Sep04:\*

1: genSeqP1980s:\*

2: genSeqP1990s:\*

3: genSeqP1000s:\*

4: genSeqP2001s:\*

5: genSeqP2002s:\*

6: genSeqP1003as:\*

7: genSeqP2003bs:\*

8: genSeqP2004s:\*

#### ALIGNMENTS

RESULT 1  
ID AAB10686 Standard; peptide; 47 AA.

ID AAB10686;

AC XX

DT 19-JAN-2001 (first entry)

DE HIV-1 regulatory virus protein R peptide svpr1-47.

XX

KW Regulatory virus protein R; Vpr; antiviral; gene therapy; pathogenicity; structural analysis; cell cycle arrest.

OS Synthetic.

XX Human immunodeficiency virus 1.

XX Key Location/Qualifiers

FT Modified-site 47

/note= "C-terminal amide"

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	262	100.0	47	3	AAB10686		Aab10686 HIV-1 reg
2	262	100.0	60	7	ABR42471		Abr42471 HIV viral
3	262	100.0	79	2	AAR48961		Aar48961 NL4-3 VPR
4	262	100.0	96	2	AAR48963		Aar48963 HIV VPR
5	262	100.0	96	2	AAW53040		Aaw53040 HIV-1 pol
6	262	100.0	96	3	AAB10049		Aab10049 HIV-1 vpr
7	262	100.0	96	3	AAB10685		Aab10685 HIV-1 reg
8	262	100.0	96	5	AAE16129		Aae16129 Human imm
9	262	100.0	96	5	ABP56175		Abp56175 HIV-1 vir
10	262	100.0	96	7	ADD01277		Adf01277 HIV-1 vpr
11	262	100.0	96	8	ADP46812		Adp46812 HIV-1 vpr
12	262	100.0	96	8	ABM79669		Abm79669 HIV-1 vpr
13	255	97.3	96	6	ABR55491		Abr55491 Amido aci
14	255	97.3	96	3	AAB69306		Aab69306 HIV-1 non
15	252	96.2	96	5	AAU080387		Aau080387 HIV-1 vpr
16	251	95.8	78	2	AAW99828		Aaw99828 HIV XKB2
17	251	95.8	96	2	AAW99823		Aaw99823 HIV L688
18	251	95.8	96	2	AAW99824		Aaw99824 HIV H71C
19	251	95.8	96	2	AAW99821		Aaw99821 HIV L64S
20	251	95.8	96	2	AAW99826		Aaw99826 HIV G75A
21	251	95.8	96	2	AAW99820		Aaw99820 HIV A59P
22	251	95.8	96	2	AAW99825		Aaw99825 HIV H71Y
23	251	95.8	96	2	AAW99827		Aaw99827 HIV C76S
24	251	95.8	96	2	AAW99815		Aaw99815 HIV vpr w
25	251	95.8	96	2	AAW99822		Aaw99822 HIV L67S

This invention describes novel synthetic peptides (1) derived from the

regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-1) which have antiviral activity and can be used for gene therapy, (1) is used for therapeutic and/or diagnostic purposes, especially in biological assays, for development of serological tests or enzyme-linked

ADN6417 HIV proteo  
Aar94544 Native Vp  
Aav99818 HIV A30S  
Adp20070 Human imm  
Aap91048 Transcript  
Adp20078 Human imm  
Aapb1856 Sequence  
Aar10174 Rap (R) P  
Aaw99819 HIV A30L

AAQ30520 HIV vpr m  
AAQ30521 HIV vpr m  
AAQ30515 HIV vpr m  
AAQ30516 HIV vpr m  
AAQ30519 HIV vpr m  
AAQ30517 HIV vpr m  
AAQ30518 HIV vpr m  
AAQ30520 HIV vpr m  
ADN6417 HIV proteo  
Aar94544 Native Vp  
Aav99818 HIV A30S  
Adp20070 Human imm  
Aap91048 Transcript  
Adp20078 Human imm  
Aapb1856 Sequence  
Aar10174 Rap (R) P  
Aaw99819 HIV A30L

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

RESULT 1  
ID AAB10686 Standard; peptide; 47 AA.

ID AAB10686;

AC XX

DT 19-JAN-2001 (first entry)

DE HIV-1 regulatory virus protein R peptide svpr1-47.

XX

KW Regulatory virus protein R; Vpr; antiviral; gene therapy; pathogenicity; structural analysis; cell cycle arrest.

OS Synthetic.

XX Human immunodeficiency virus 1.

XX Key Location/Qualifiers

FT Modified-site 47

/note= "C-terminal amide"

XX

PN WO20049038-A2.

XX

PD 24-AUG-2000.

XX

PR 19-FEB-2000; 2000WO-DE000525.

XX

PR 19-FEB-1999; 93DE-01008752.

XX

PR 19-FEB-1999; 93DE-01008766.

XX

PA (SCHU/); SCHUBERT U.

PA (HENK/); HENKLEIN P.

PA (WRAY/); WRAY V.

XX

PA Schubert U, Henklein P, Wray V;

XX

DR WPT; 2000-565367/52.

XX

PT New synthetic peptides from the Vpr protein of human immune deficiency in

water.

XX

Claim 3.2; Page 5; 35pp; German.

XX

CC This invention describes novel synthetic peptides (1) derived from the

regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-

1) which have antiviral activity and can be used for gene therapy, (1) is

used for therapeutic and/or diagnostic purposes, especially in biological

assays, for development of serological tests or enzyme-linked

CC immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in  
 CC blood), to raise specific antibodies and antisera (especially those  
 CC reactive with specific epitopes), and as antiviral agents. (1) can also  
 CC be used in screening for potential Vpr antagonists (i.e. compounds that  
 CC modulate interaction of Vpr with cellular factors, transcription-  
 CC activating properties of Vpr, transport of Vpr and its incorporation into  
 CC viral particles, Vpr-induced cell cycle arrest, and cytotoxic and ion-  
 CC channel activities of Vpr). (1) is used to establish cell or animal  
 CC models for studying pathogenicity of Vpr, for structural analysis of Vpr  
 CC and its domains, for *in vitro* assembly of new vectors for gene therapy,  
 CC *in vitro* or *in vivo*, for complementing the function of Vpr-defect mutants  
 CC in cell cultures, and to reduce flexibility of Vpr induced by the N-  
 CC terminal domain. Synthetic (1), are soluble in water and can be  
 CC formulated as highly concentrated solutions (molar) without protein  
 CC aggregation, so are well suited to analysis by nuclear magnetic  
 CC resonance, X-ray or circular dichroism techniques. (1) adopt a folded  
 CC structure, have biological activity comparable to that of viral Vpr, and  
 CC can be produced, at high purity, on the milligram scale. This sequence  
 CC represents the synthetic HIV-1 derived Vpr peptide *svpr1-47* which is used  
 CC in the method of the invention

The present sequence is that of amino acids 1-60 of HIV viral protein R (Vpr, also called lentiviral R protein). Vpr is incorporated into the HIV virion and helps to target the viral preintegration complex to the nucleus in nondividing cells through its nuclear localisation signal. It is also responsible for arresting HIV infected cells in the G2 phase of the cell cycle, which results in increased virus production. The invention provides methods for identifying compounds that induce loss of Vpr in a eukaryotic cell, and methods for identifying compounds that inhibit a peptidyl-prolyl cis-trans isomerase activity of a protein that catalyses cis-trans isomerization of cis-peptidyl prolyl bonds in Vpr. Such compounds are useful for treating lentiviral infections, including HIV infections.

```

2 Sequence 60 AA;
3 Query Match 100.0%; Score 262; DB 7; Length 60;
4 Best Local Similarity 100.0%; Pred. No. 3.e-26;
5 Matches 47; Conservative 0; Mismatches 0;
6 Indels 0; Gaps 0;

```

RESULT 3  
AAR48961  
AAR48961 standard; protein; 79 AA.  
1 MEOAPEDGQPQREPYNWTLLEELKSEAVRHFPRIWHLNLGQH<sup>Y</sup> 47

25-MAR-2003 (revised)  
12-SEP-1994 (first entry)

HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection; naturally occurring virus; NOV; translation; replication; infectivity; homologous; B HIV; SIV; filoviruses; PBC; homologous B HIV; SIV; filoviruses; PBC

WO9403596-A1  
Synthetic.

17-FEB-1994 .  
30-JUL-1993 /  
93WO-US007179 .

30-JUL-1992; 92US-00922104.  
(UYHA-) UNIV HAWAII.

ru w , wang j ;  
WBI ; 1994-05685/08 .  
N-PSDB ; AAQ7688 .

New antisense viruses and anti-sense-ribozyme viruses - used for treating or preventing viral infections, paticic. HIV-1, HIV-2 or SIV infection.

This sequence is encoded by a PCR fragment of NI4-3 and represents the N-terminal peptide fragment of the full length VPR protein. The DNA encoding this fragment was ligated into Cla I/Sal I digested pX and the corresponding plasmid was used to produce the antisense virus of the invention. Antisense or truncated RNAs expressed by these viruses bind to the mRNAs expressed by the naturally occurring viruses (NOVs) and prevent the mRNAs from being translated into proteins, thereby preventing the NOVs from replicating. The antisense viruses maintain the infectivity of the NOVs, allowing antisense RNAs to reach the mRNAs of the natural viruses. Antisense viruses such as these may be used for treating or preventing a

CC B infection. (Updated on 25-MAR-2003 to correct PN field.)  
 SQ Sequence 79 AA;  
 Query Match 100.0%; Score 262; DB 2; Length 79;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PS 1 MEQAPEDQGQREPYNNEWTLEELKSEAVRHFRWLHNGLQHIV 47  
 DB 1 MEQAPEDQGQREPYNNEWTLEELKSEAVRHFRWLHNGLQHIV 47

RESULT 4  
 AAR8963 ID AAR8963 standard; protein: 96 AA.  
 XX AAR8963;  
 AC XX  
 DT 25-MAR-2003 (revised)  
 DT 12-SEP-1994 (first entry)  
 DE HIV VPR.  
 XX HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;  
 KW naturally occurring virus; NOV; translation; replication; infectivity;  
 KW hepatitis B; HIV-2; SIV; flip-over PCR.  
 XX Synthetic.  
 OS WO9403596-A1.  
 XX PD 17-FEB-1994.  
 PF 30-JUL-1993; 93WO-US007179.  
 PR 30-JUL-1992; 92US-00921104.  
 PA (UHFA-) UNIV HAWAII.  
 XX Hu W, Wang J;  
 PI XX  
 DR WPI:1994-065685/08.  
 N-PSDB; AAQ48962.  
 PT New antisense viruses and anti:sense-ribozyme viruses - used for treating  
 or preventing viral infections, partic. HIV-1, HIV-2 or SIV infection.  
 Disclosure; Page 111; 167pp; English.

This sequence represents the "perfect" VPR protein encoded by the PCR  
 fragment of PX-CS which encodes the truncated gag gene and the "perfect"  
 vpr gene. The cDNA fragment encoding this protein was used to produce the  
 antisense virus of the invention. Antisense or truncated RNAs expressed  
 by these viruses bind to the mRNAs expressed by the naturally occurring  
 viruses (NOVs) and prevent the mRNAs from being translated into proteins,  
 thereby preventing the NOV from replicating. The antisense viruses  
 maintain the infectivity of the NOVs, allowing antisense RNAs to reach  
 the mRNAs of the natural viruses. Antisense viruses such as these may be  
 used for treating or preventing a viral infection, particulary HIV-1,  
 HIV-2 or SIV infection or hepatitis B infection. (Updated on 25-MAR-2003  
 to correct PN field.)  
 SQ Sequence 96 AA;

Query Match 100.0%; Score 262; DB 2; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PS 1 MEQAPEDQGQREPYNNEWTLEELKSEAVRHFRWLHNGLQHIV 47  
 DB 1 MEQAPEDQGQREPYNNEWTLEELKSEAVRHFRWLHNGLQHIV 47

RESULT 5  
 AAW53040 ID AAW53040 standard; peptide; 96 AA.  
 XX AAW53040;  
 AC XX  
 DT 17-OCT-2003 (revised)  
 DT 17-JUL-1998 (first entry)  
 DE HIV-1 polypeptide.  
 XX Recombinant plant virus; HIV-1; protein production; immunisation;  
 KW fusion capsid protein; alfalfa mosaic virus; larvirus; pathogen;  
 KW rhadovirus.  
 XX Human immunodeficiency virus 1.  
 OS XX  
 PN WO9808375-A1.  
 XX PD 05-MAR-1998.  
 PF 28-AUG-1997; 97WO-US015200.  
 XX PR 28-AUG-1996; 96US-00704856.  
 PA (UJJE-) UNIV JEFFERSON THOMAS.  
 PI XX  
 DR Koprowski H, Hooper DC, Yusibov V, Modelski A;  
 XX WPI; 1998-179070/16.  
 PT Production of poly:peptide(s), particularly for use in vaccines - by  
 expression as fusion proteins with plant virus capsid protein in plant  
 cells infected with virus.  
 Disclosure; Page 4; 63pp; English.  
 XX  
 CC This sequence is a HIV-1 polypeptide that can be used in a recombinant  
 plant virus used in the process of the invention. The process is for  
 administering a polypeptide to an animal comprising: (a) infecting a  
 plant cell with recombinant plant virus nucleic acid that will be  
 processed in a plant cell to produce a fusion capsid protein (FCP), the  
 FCP comprises a plant virus capsid protein (PvCP) and a polypeptide that  
 is not a PvCP, the PvCP being an alfalfa mosaic virus (AlMV) capsid  
 protein (CP) or larvirus CP thereby creating a infected cell; (b)  
 cultivating the infected cell, or a derivative cell derived from the  
 infected cell, under conditions where the infected cell or derivative  
 cell makes the FCP; and (c) administering the FCP or a portion to an  
 animal. The recombinant plant virus can also be used for production of  
 polypeptides. The method is used particularly for the production of  
 CC polypeptides which can be used for immunisation against pathogens such as  
 CC rhabdovirus or HIV. (Updated on 17-OCT-2003 to standardise OS field)  
 XX Sequence 96 AA;  
 SQ Query Match 100.0%; Score 262; DB 2; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PS 1 MEQAPEDQGQREPYNNEWTLEELKSEAVRHFRWLHNGLQHIV 47  
 DB 1 MEQAPEDQGQREPYNNEWTLEELKSEAVRHFRWLHNGLQHIV 47

RESULT 6  
 AAB10049 ID AAB10049 standard; protein; 96 AA.  
 AC XX  
 DT 12-SEP-2003 (revised)  
 DT 02-NOV-2000 (first entry)



OS	Human immunodeficiency virus 1.	ABP56175	ABP56175 standard; peptide; 96 AA.
PH	Key Location/Qualifiers	XX	XX
FT	Region 17 .29	AC	AC ABP56175;
FT	/label= Alpha_1_helix	XX	
FT	36 .47	DT	29-AUG-2003 (revised)
FT	/label= Alpha_2_helix	DT	28-MAR-2003 (first entry)
FT	53 .78	XX	
FT	/label= Alpha_3_helix	DE	HTV-1 viral protein R (Vpr) amino acid sequence.
XX	WO200190159-A2.	XX	XX
XX	PR 29-NOV-2001.	KW	Mitochondrial membrane permeabilisation; mitochondrion; PTPC; permeability transition pore complex; virucide; neuroprotective; vasoconstrictive; cytostatic; infection; cell death regulation; apoptosis; mitochondrial permeability transition pore complex modulator; cancer; apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.
XX	PF 23-MAY-2001; 2001WO-US016943.	KW	
XX	PR 23-MAY-2000; 2000US-0205610P.	KW	
PR 09-FEB-2001; 2001US-0267827P.	XX		
PR 20-APR-2001; 2001US-0083932P.	XX		
XX	PA (GLADSTONE INST J DAVID.	XX	
PA (SCHUTU) SCHUBERT U.	XX	PD	08-AUG-2002.
(HENK/)	(HENK/)	PP	01-FEB-2002; 2002WO-EP001633.
XX	PI Schubert U, Henklein P, Sherman MP, Greene WC, De Noronha CMC;	XX	
XX	WPI; 2002-083087/11.	PR	02-FEB-2001; 2001US-0265594P.
XX	DR	XX	
PS	Example 1; FIG 1A; 72pp; English.	PA	(INSP ) INST PASTEUR.
XX	The present invention relates to compositions comprising Vpr polypeptides conjugated to a therapeutic molecule. Vpr polypeptides are regulatory or auxiliary proteins encoded by a lentivirus, human immunodeficiency virus type 1 (HIV-1). The invention also relates to a method for delivering a molecule into a cell which comprises contacting the cell with a conjugate comprising a Vpr polypeptide conjugated to the molecule. The method is useful for delivering a polypeptide, polynucleotide (DNA or RNA) or a toxin into a cell. Preferably, a cancer cell, or a cell infected with a pathogen such as lentivirus, HIV or retrovirus, bacterium or a parasite. Compositions comprising Vpr polypeptides conjugated to a toxin is useful for killing a cancer cell or a cell infected with a pathogen where the toxin is further conjugated to a regulatory molecule and the contact with the target cell exerts an effect on the regulatory molecule that results in activation of the toxin. The method is useful for inhibiting cell proliferation and treating a disorder associated with dysregulated cell growth in a subject. Vpr polypeptides when administered alone are useful for increasing sensitivity to radiation therapy in a subject undergoing radiation therapy. They can also be used to treat hyperproliferative cell disorders such as malignancies, psoriasis and other disorders associated with dysregulated cell growth. Vpr polypeptides conjugated to a regulatory moiety is useful for modulating the expression of a transgene in a cell. Vpr polypeptides alone or conjugated to an antigen is useful for increasing an immune response. The present sequence is synthetic Vpr (sVpr) protein from HIV-1. (updated on 29-AUG-2003 to standardise OS field)	(CNRS ) CENT NAT RECH SCI.	
XX	PS	XX	
CC	Delivering molecule into cell for inhibiting cell proliferation and killing target cell, comprises contacting cell with Vpr polypeptide, regulatory protein encoded by HIV type 1, alone or conjugated to molecule.	PI	Edelman L, Jacotot E, Briand J;
PT	XX	XX	
PT	DR	DR	WPI; 2002-619260/66.
XX	PS	XX	
PT	Example 1; FIG 1A; 72pp; English.	PT	New chimeric bifunctional molecules that target specific cells and regulate the apoptosis function of the permeability transition pore complex of the mitochondria, useful for treating or preventing e.g. cancer or ischaemia.
PT	XX	PT	
PT	PS Disclosure; Page 13; 76pp; English.	PT	
XX	CC	CC	The present invention describes a chimeric bifunctional molecule (I) comprising at least a first functional molecule covalently linked to a second functional molecule, which is able to modulate the activity of the permeability transition pore complex (PTPC) of the mitochondria. (I) has the function of specifically targeting and entering a tissue cell
CC	CC	CC	population. The second functional molecule has the function of specifically targeting and inducing or preventing the death of the cells by apoptosis by regulating the opening or the closing of the PTPC of the mitochondria or its fragment. (I) has virucide, neuroprotective, vasoconstrictive and cytostatic activities, and can be used as a mitochondrial permeability transition pore complex (PTPC) modulator. (I) is useful for treating or preventing a pathological infection or disease. (I) is also useful for regulating cell death regulatory molecules, specifically the apoptogenic function of the PTPC, for treating e.g. cancer, ischaemia, neurodegenerative diseases, fulminant hepatitis or viral infections. The present sequence represents the HIV-1 viral protein R (Vpr) amino acid sequence, which is given in the exemplification of the present invention.
CC	CC	CC	(Updated on 29-AUG-2003 to standardise OS field)
CC	CC	CC	Sequence 96 AA;
SQ	Sequence 96 AA;	XX	Sequence 96 AA;
Query Match	100.0%	Score 262;	DB 5;
Best Local Similarity	100.0%	Length 96;	Length 96;
Matches 47;	Conservative 0;	Mismatches 0;	Indels 0;
Qy	1 MEQAPEDQGPQRGPYNEWTLEELBELKSAVRHPRFLHNQHQHY 47	Db	1 MEQAPEDQGPQRGPYNEWTLEELBELKSAVRHPRFLHNQHQHY 47
Db	1 MEQAPEDQGPQRGPYNEWTLEELBELKSAVRHPRFLHNQHQHY 47	RESULT 9	
		ADD01277	ADD01277 standard; protein; 96 AA.



XX Human immunodeficiency virus type 1.  
 OS WO2003076621-A2.  
 PN 18-SEP-2003.  
 PD 07-MAR-2003; 2003WO-CA000325.  
 XX PR 08-MAR-2002; 2002US-0362384P.  
 PA (UNMO-) UNIV MONTREAL.  
 PI Cohen EA, Yao X, Belhumeur P, Lemay J;  
 XX DR WPI; 2004-042337/04.  
 New polypeptides that bind to viral Vpr protein, useful for treatment, prevention, diagnosis and prognosis of immune deficiency virus infection.  
 Example 20; Page 33-34; 143DP; English.  
 CC The present invention relates to peptide which are capable of binding to the HIV protein Vpr and/or modulates Vpr-related activity. Such peptides are used for prevention, treatment, diagnosis and prognosis of Vpr-related diseases, particularly lentiviral infection (specifically HIV-1 or -2, or simian immune deficiency virus), for modulating, particularly inhibiting, Vpr-related activities and for detecting Vpr in a sample. Nucleic acids encoding such peptides and cells that contain this nucleic acid can also be used therapeutically. The present sequence is a protein of relevance to the invention  
 XX Sequence 96 AA;  
 SQ Query Match 100.0%; Score 262; DB 8; Length 96;  
 Best Local Similarity 100.0%; Prod. No. 6.e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 YY 1 MEQAPEDQGPQREPYNNEWTLEELBLKSEAVRHPRIMHLGQHY 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELBLKSEAVRHPRIMHLGQHY 47

RESULT 13  
 ABR55491 ID ABR55491. standard; protein; 96 AA.  
 AC ABR55491;  
 XX DT 11-AUG-2003 (first entry)  
 XX Human immunodeficiency virus.  
 DE Amino acid sequence of a HIV vpr protein.  
 XX KW Polymorphic marker; host response; HIV; AIDS related virus; vaccine;  
 KW hepatitis related virus; HCV; HBV; drug resistance; vpr.  
 OS XX  
 PN WO2003035097-A1.  
 XX PR 23-OCT-2002; 2002WO-AU0001450.  
 XX PD 01-MAY-2003.  
 XX PF 23-OCT-2002; 2002AU-00008425.  
 PA (EPIP-) EPIPOP PTY LTD.  
 PI Mallal S;  
 XX DR WPI; 2003-449231/42.  
 XX PR Determining the influence of variation in host genes on the selection of

XX microorganisms with protein substitutions, comprises typing individuals of a cohort infected with a microorganism for an intrinsic polymorphic marker.  
 PT PT  
 XX PS Claim 22; Page 89; 157BP; English.  
 XX CC The specification describes method of determining the influence of variation in host genes on selection of microorganisms with protein substitutions. The method comprises typing all individuals of a population of patients infected with a microorganism for at least one selected intrinsic polymorphic marker involved in the host response to the presence of the microorganism. The method is useful for examining selective pressures confronting a wide range of organisms that exhibit pathogenic traits in a host, such as bacteria, fungi, mycobacterium, viruses and virus-like particles. For examining microorganisms that have adapted to evolve rapidly, including HIV and AIDS related viruses and the hepatitis related viruses such as HCV and HBV. The method is useful for designing a vaccine to prevent or delay the emergence of drug resistance in patients treated with a particular drug specific for a microorganism where the drug affects the replication of the microorganism at the nucleotide or amino acid level. The present sequence represents a HIV vpr protein, which is expected to provide optimal cytotoxic T lymphocyte (CTL) induced therapeutic protection to the cohort examined in that study  
 XX SQ Sequence 96 AA;  
 CC Query Match 97.7%; Score 256; DB 6; Length 96;  
 CC Best Local Similarity 97.9%; Prod. No. 3.9e-25;  
 CC Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 YY 1 MEQAPEDQGPQREPYNNEWTLEELBLKSEAVRHPRIMHLGQHY 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELBLKSEAVRHPRIMHLGQHY 47

RESULT 14  
 AAB69306 ID AAB69306 standard; protein; 96 AA.  
 XX AC AAB69306;  
 XX DT 12-SEP-2003 (revised)  
 DT 20-APR-2001 (first entry)  
 XX DB HIV-1 non-subtype B clone 93BR029-4 vpr protein.  
 XX KW HIV-1; human immunodeficiency virus; non-subtype B; gag; pol; env; vpu; vif; vpr; tat; rev; nef; vaccine.  
 XX OS Human immunodeficiency virus 1.  
 XX PN WO20026416-A1.  
 XX PR 02-NOV-1998; 98US-00184418.  
 XX PA (UABR-) UAB RES FOUND.  
 XX PI Hahn BH, Shaw GM, Gao F;  
 XX DR WPI; 2000-365651/31.  
 XX PR Novel genomic nucleic acids of non-subtype B human immunodeficiency virus type 1 useful for detecting and treating AIDS comprises a specific nucleotide sequence.  
 XX PS Claim 41; Fig 17; 131PP; English.  
 XX CC The present invention provides the protein and coding sequences for a number of human immunodeficiency virus (HIV) type 1 non-subtype B

CC isolates. The sequences shown include the near full-length coding  
 CC sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat,  
 CC rev and nef proteins. These can be used to detect the presence of HIV-1  
 CC in a sample and to produce antibodies against non-subtype B HIV-1 virus.  
 CC These antibodies can be used in vaccines to prevent and treat HIV  
 CC infection. (Updated on 12-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 96 AA;

Query Match 97.3%; Score 255; DB 3; Length 96;  
 Best Local Similarity 95.7%; Pred. No. 5.3e-25;  
 Matches 45; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRLWNLGQHYY 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRLWNLGQHYY 47

## RESULT 15

AAU80187  
 ID AAU80187 standard; protein; 96 AA.

XX  
 AC AAU80187;

XX  
 DT 29-AUG-2003 (revised)

DT 15-JUL-2002 (first entry)

XX  
 DE HIV-1 Vpr protein.

XX  
 KW HIV-1; acquired immunodeficiency syndrome; AIDS; vpr.

XX  
 OS Human immunodeficiency virus 1.

XX  
 PH

Key Location/Qualifiers  
 PT Misc-difference 45  
 FT /note= "Encoded by CAA"

XX  
 JP2002085099-A.

PN  
 PD 26-MAR-2002.

XX  
 PP 14-SEP-2000; 20000JP-00280851.

XX  
 PR 14-SEP-2000; 20000JP-00280851.

XX  
 PA (KOKU-) KOKURITSU YOBO EISRI KENKUSHO.

PA (ORIY ) ORIENTAL YEAST CO LTD.

XX  
 DR 2002-378279/41.

DR N-PSDB; ABK50386.

XX  
 PT Detection of immunodeficiency virus by detecting the presence of Vpr

protein.

XX  
 PS Disclosure; Page 8; 17pp; Japanese.

CC The invention relates to a method for detecting immunodeficiency virus in  
 CC a sample in which the presence of Vpr (not defined) protein in the sample  
 CC is detected. Also included are a kit for use in the above detecting  
 CC method containing a cell and a pigment, and a method for screening a  
 CC compound promoting or inhibiting the intake of a substance having a  
 CC molecular weight (M.W.) of 300 to 3000 in which the promotion or the  
 CC inhibition of intake of the substance by the presence of a test compound  
 CC is used as the index in the intake of the substance to the cell by a  
 CC treatment using a sample containing Vpr protein. The method is used for  
 CC detecting immunodeficiency virus (e.g. Human immunodeficiency virus-1,  
 CC the causative agent of acquired immunodeficiency virus syndrome, AIDS) in  
 CC a sample. The present sequence represents HIV-1 Vpr. (Updated on 29-AUG-  
 CC 2003 to standardise OS field)

XX  
 SQ Sequence 96 AA;

Query Match 96.2%; Score 252; DB 5; Length 96;

Best Local Similarity 97.9%; Pred. No. 1.3e-24;  
 Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRLWNLGQHYY 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRLWNLGQHYY 47

Search completed; October 18, 2004, 18:45:32  
 Job time : 63.6675 secs

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2004, 18:42:45 ; Search time 27.4167 Seconds  
(without alignments)

113.688 Million cell updates/sec

Title: US-09-913-927D-2

Perfect score: 262

Sequence: 1 MEQAPEDQGPOREPYNEWTL.....SEAVRFHPPRIWLHNIGQHIV 47

Scoring table: BILOSUM62

Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6.ptodata/1/iaa/5A COMB.pep:\*

2: /cgn2\_6.ptodata/1/iaa/5B COMB.pep:\*

3: /cgn2\_6.ptodata/1/iaa/6A COMB.pep:\*

4: /cgn2\_6.ptodata/1/iaa/6B COMB.pep:\*

5: /cgn2\_6.ptodata/1/iaa/8C PCTU COMB.pep:\*

6: /cgn2\_6.ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	262	100.0	96	4	US-09-309-572-19	Sequence 19, App1
2	262	100.0	96	4	US-09-718-096-19	Sequence 19, App1
3	252	96.2	96	3	US-08-704-856C-15	Sequence 15, App1
4	252	96.2	96	4	US-09-242-881-15	Sequence 1, App1
5	249	95.0	96	4	US-09-839-329-1	Sequence 4, App1
6	248	94.7	72	2	US-08-301-915-4	Sequence 4, App1
7	248	94.7	72	3	US-08-524-694A-4	Sequence 5, App1
8	248	94.7	72	4	US-09-454-156A-4	Sequence 4, App1
9	248	94.7	78	3	US-09-124-900-5	Sequence 1, App1
10	248	94.7	96	3	US-08-301-915-1	Sequence 1, App1
11	248	94.7	96	4	US-08-524-694A-1	Sequence 1, App1
12	248	94.7	96	4	US-09-454-156A-1	Sequence 10, App1
13	238	90.8	95	4	US-09-319-588C-10	Sequence 11, App1
14	220	84.0	100	4	US-09-462-917A-16	Sequence 115, App1
15	209	79.8	100	4	US-09-462-917A-15	Sequence 117, App1
16	206	78.5	93	4	US-09-462-917A-17	Sequence 118, App1
17	194	74.0	100	4	US-09-462-917A-18	Sequence 49, App1
18	138	52.7	100	4	US-09-206-551-49	Patent No. 5223423
19	118	45.0	3077	6	5223423-2	Sequence 2, App1
20	111	42.4	105	6	US-08-301-915-2	Sequence 2, App1
21	111	42.4	105	3	US-08-524-694A-2	Sequence 2, App1
22	111	42.4	105	4	US-09-454-156A-2	Sequence 8, App1
23	110	42.0	20	3	US-09-055-075C-8	Sequence 8, App1
24	110	42.0	20	4	US-09-919-124-8	Sequence 8, App1
25	110	42.0	21	5	PCT-US94-02191-4	Sequence 4, App1
26	103	39.3	105	3	US-08-659-251-9	Sequence 9, App1
27	103	39.3	105	3	US-09-256-490-9	Sequence 9, App1

ALIGNMENTS

RESULT 1

US-09-309-572-19

; Sequence 19, Application US/09309572

; Patent No. 6440730

; GENERAL INFORMATION:

; APPLICANT: Heinrich-Pette-Institut

; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV

; FILE REFERENCE: P50489

; CURRENT APPLICATION NUMBER: US/09/309,572

; CURRENT FILING DATE: 1999-05-11

; EARLIER APPLICATION NUMBER: DE 198 56 463

; EARLIER FILING DATE: 1998-11-26

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

; FEATURE:

; OTHER INFORMATION: vpr protein

US-09-309-572-19

Query Match 100.0% ; Score 262; DB 4; Length 96;

Best Local Similarity 100.0%; Pred. No. 1.8E-27;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPOREPYNEWTLLEELKSEAVRFHPPRIWLHNIGQHIV 47

Db 1 MEQAPEDQGPQRPYNEWTLLEELKSEAVRFHPPRIWLHNIGQHIV 47

RESULT 2

US-09-718-096-19

; Sequence 19, Application US/097180936

; Patent No. 6589763

; GENERAL INFORMATION:

; APPLICANT: Von Laer, Meike-Dorothee

; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV

; FILE REFERENCE: 35-195

; CURRENT APPLICATION NUMBER: US/09/718-096-19

; PRIORITY APPLICATION NUMBER: DE 19856463.5

; PRIORITY APPLICATION NUMBER: EP 99250415.9

; PRIORITY APPLICATION NUMBER: EP 99250415.9

; PRIORITY APPLICATION NUMBER: US 09/309,572

; PRIORITY APPLICATION NUMBER: 1999-11-25

; PRIORITY APPLICATION NUMBER: US 09/309,572

; PRIORITY FILING DATE: 1998-11-26

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

LENGTH: 96  
 TYPE: PRT  
 ORGANISM: Human immunodeficiency virus type 1  
 FEATURE: vpr protein  
 OTHER INFORMATION: vpr protein  
 US-09-718-096-19

Query Match 100.0%; Score 262; DB 4; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 1.0e-27;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGQREPYNNEWTLEELKSEAVRHFPRIWLNGQHLY 47  
 Db 1 MEQAPEDQGQREPYNNEWTLEELKSEAVRHFPRIWLNGQHLY 47

---

RESULT 3  
 US-08-704-856C-15  
 Sequence 15, Application US/08704856C

GENERAL INFORMATION:  
 APPLICANT: Koprowski, Hilary  
 APPLICANT: Yusibov, Vidadi  
 APPLICANT: Hooper, Douglas C.  
 APPLICANT: Modeliska, Anna

TITLE OF INVENTION: Polypeptides Fused with Plant Virus  
 TITLE OF INVENTION: Coat Proteins

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Allan H. Fried & Associates  
 STREET: 1525 Locust Street, 15th Floor  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTY: USA  
 ZIP: 19102

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Corel WordPerfect

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/242,881  
 FILING DATE: 25-Feb-1999  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/704,856  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fried, Allan H.  
 REGISTRATION NUMBER: 31,253  
 REFERENCE/DOCKET NUMBER: T19-007  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 732-7090  
 TELEFAX: (215) 732-7090  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 HYPOTHETICAL: N

US-09-242-881-15

Query Match 96.2%; Score 252; DB 4; Length 96;  
 Best Local Similarity 95.7%; Pred. No. 3.9e-26;  
 Matches 45; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGQREPYNNEWTLEELKSEAVRHFPRIWLNGQHLY 47  
 Db 1 MEQAPEDQGQREPYNNEWTLEELKSEAVRHFPRIWLNGQHLY 47

RESULT 5  
 US-09-839-329-1  
 Sequence 1, Application US/09839329

GENERAL INFORMATION:  
 APPLICANT: Michael P. Sherman  
 APPLICANT: Warner C. Greene  
 APPLICANT: Carlos M.C. de No. 6664040ohna  
 APPLICANT: Ulrich Schubert  
 APPLICANT: Peter Henklein

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF  
 A MOLECULE INTO A CELL

FILE REFERENCE: G&C 30448.91-US-U2  
 CURRENT APPLICATION NUMBER: US/09/839,329  
 PRIOR APPLICATION NUMBER: 60/206,610  
 PRIOR FILING DATE: 2000-05-23  
 CURRENT FILING DATE: 2001-04-20  
 PRIOR APPLICATION NUMBER: 60/267,827  
 PRIOR FILING DATE: 2001-02-09  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 1

---

RESULT 4  
 US-09-242-881-15  
 Sequence 15, Application US/09242881  
 APPLICANT: General Information:

LENGTH: 96  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic peptide of regulatory virus proteins R  
 OTHER INFORMATION: (vpr) of human immunodeficiency virus type 1  
 OTHER INFORMATION: (HIV-1)  
 US-09-839-329-1

Query Match 95.0%; Score 249; DB 4; Length 96;  
 Best Local Similarity 97.9%; Pred. No. 9.3e-26;  
 Matches 46; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
 NUMBER OF SEQUENCES: 5

1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPPRILWNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPPRILWNLGQHIV 47

RESULT 7  
 US-08-301-915-4  
 Sequence 4, Application US/08301915  
 Patent No. 5861161  
 GENERAL INFORMATION:  
 APPLICANT: COHEN, Eric A.  
 APPLICANT: BERGERON, Dominique  
 APPLICANT: CHECROUNE, Florent  
 APPLICANT: YAO, Xiao-Jian  
 APPLICANT: PIGNAC-KOBINGER, Gary  
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED ON HIV-1 VPR FUSION MOLECULES  
 CURRENT APPLICATION DATA:  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KLAUBER & JACKSON  
 STREET: Continental Plaza, 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: N.J.  
 COUNTRY: U.S.A.  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/524,694A  
 FILING DATE: September 7, 1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JACKSON, David A.  
 REGISTRATION NUMBER: 26,742  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1584  
 TELEX: 133521  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 72 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 US-08-524-694-4

Query Match 94.7%; Score 248; DB 3; Length 72;  
 Best Local Similarity 94.6%; Pred. No. 9.3e-26;  
 Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 NUMBER OF SEQUENCES: 5

1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPPRILWNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPPRILWNLGQHIV 47

RESULT 8  
 US-09-454-156A-4  
 Sequence 4, Application US/09454156A  
 Patent No. 6466539  
 GENERAL INFORMATION:  
 APPLICANT: COHEN, Eric A.  
 APPLICANT: BERGERON, Dominique  
 APPLICANT: CHECROUNE, Florent  
 APPLICANT: YAO, Xiao-Jian  
 APPLICANT: PIGNAC-KOBINGER, Gary  
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED ON HIV-1 VPR FUSION MOLECULES  
 CURRENT APPLICATION DATA:  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KLAUBER & JACKSON  
 STREET: Continental Plaza, 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: N.J.

COUNTRY: U.S.A.  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentnet Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/454,156A  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/301,915  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JACKSON, David A.  
 TELECOMMUNICATION INFORMATION:  
 REGISTRATION NUMBER: 26,742  
 TELEPHONE: 201-487-5800  
 TELEX: 133521  
 FILING DATE:  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 72 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 US-09-454-156A-4

Query Match Score 248; DB 4; Length 72;  
 Best Local Similarity 93.6%; Pred. No. 9.3e-26; Mismatches 1; Indels 0; Gaps 0;  
 US-09-454-156A-4

Query Match Score 248; DB 2; Length 96;  
 Best Local Similarity 93.6%; Pred. No. 1.3e-25; Mismatches 2; Indels 0; Gaps 0;  
 US-09-454-156A-4

RESULT 9  
 US-09-124-900-5  
 Sequence 5, Application US/09124900  
 Patent No. 6268484  
 GENERAL INFORMATION:  
 APPLICANT: KATINGER, Hermann  
 APPLICANT: BUCHACHER, Andrea  
 APPLICANT: ERNST, Wolfgang  
 APPLICANT: BAILAUN, Claudia  
 APPLICANT: PURTSCHER, Martin  
 APPLICANT: TRKOLA, Alexandra  
 APPLICANT: PREDL, Renate  
 APPLICANT: SCHMATZ, Christine  
 APPLICANT: KLIMA, Annelies  
 APPLICANT: STEINDL, Franz  
 APPLICANT: MUSTER, Thomas  
 TITLE OF INVENTION: HIV-Vaccines  
 FILE REFERENCE: 1939-112P  
 CURRENT APPLICATION NUMBER: US/09/124,900  
 CURRENT FILING DATE: 1998-07-30  
 PRIOR APPLICATION NUMBER: PCT/EP95/01481  
 PRIOR FILING DATE: 1995-04-19  
 NUMBER OF SEQ ID NOS: 11  
 SOFTWARE: Patentnet version 3.0  
 SEQ ID NO 5  
 LENGTH: 78  
 TYPE: PRT  
 US-09-124-900-5

Query Match Score 248; DB 3; Length 78;  
 Best Local Similarity 93.6%; Pred. No. 1e-25; Mismatches 1; Indels 0; Gaps 0;  
 US-09-124-900-5

RESULT 10  
 US-08-301-915-1  
 Sequence 1, Application US/08301915  
 Patent No. 5861161  
 GENERAL INFORMATION:  
 APPLICANT: COHEN, Eric A.  
 APPLICANT: BERGERON, Dominique  
 APPLICANT: CHECROUET, Florent  
 APPLICANT: YAO, Xiao-Jian  
 APPLICANT: PIGNAC-KOBINGER, Gary  
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS  
 TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CLAUBER & JACKSON  
 STREET: Continental Plaza, 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: N.J.  
 COUNTRY: U.S.A.  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/301,915  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JACKSON, David A.  
 REGISTRATION NUMBER: 26,742  
 TELEPHONE: 201-487-5800  
 TELEX: 133521  
 CLASSIFICATION: 536  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 US-08-301-915-1

Query Match Score 248; DB 2; Length 96;  
 Best Local Similarity 93.6%; Pred. No. 1.3e-25; Mismatches 2; Indels 0; Gaps 0;  
 US-08-301-915-1

RESULT 11  
 US-08-524-694A-1  
 Sequence 1, Application US/08524694A  
 Patent No. 6043081  
 GENERAL INFORMATION:  
 APPLICANT: COHEN, Eric A.  
 APPLICANT: BERGERON, Dominique  
 APPLICANT: CHECROUET, Florent  
 APPLICANT: YAO, Xiao-Jian  
 APPLICANT: PIGNAC-KOBINGER, Gary  
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS  
 TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES

```

; APPLICATION NUMBER: 08/301,915
; FILING DATE: 08/30/1991
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-454-156A1

Query Match 94.7%; Score 93.6%; Pred 2; M
Best Local Similarity 93.6%; Pred 2; M
Matches 44; Conservative 2; M
Qy 1 MEQAPEDQGPQEPYNNWTELEL
Db 1 MEQAPEDQGPQEPYNNWTELEL

RESULT 13
US-09-319-589C-10
; Sequence 10, Application US/09319588
; Patent No. 6509018
; GENERAL INFORMATION:
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: ASSISTANCE PUBLIQUE-HOPITAUX
; APPLICANT: INSTITUT PASTEUR
; APPLICANT: MAUCLIRE, Philippe
; APPLICANT: LOUSSERT-ATAKA, Ibtissa
; APPLICANT: SIMON, Francois
; APPLICANT: SARAGOSTI, Sentob
; APPLICANT: BARRE-SINOUSSI, Francois
; TITLE OF INVENTION: NON-M NON-O HIV
; FILE REFERENCE: 598US12
; CURRENT APPLICATION NUMBER: US/09/319588
; CURRENT FILING DATE: 1999-08-27
; PRIORITY APPLICATION NUMBER: FR96/1508
; PRIORITY FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 10
; TYPE: PRT
; LENGTH: 95
; ORGANISM: Human immunodeficiency virus
; US-09-319-589C-10

Query Match 90.8%; Score 89.4%; Pred 2; M
Best Local Similarity 89.4%; Pred 2; M
Matches 42; Conservative 2; M
Qy 1 MEQAPEDQGPQEPYNNWTELEL
Db 1 MERAPEDQGPQEPYNNWTELEL

RESULT 14
US-09-462-917A-116
; Sequence 116, Application US/0946291
; Patent No. 6511801
; GENERAL INFORMATION:
; APPLICANT: Delaporte, Eric
; APPLICANT: Peeters, Martine
; APPLICANT: Van den Haesevelde, Maril
; APPLICANT: Vanden Haesevelde, Maril

```

i TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof  
 i FILE REFERENCE: INNS:014 11362\_0014.NPUS00  
 i CURRENT APPLICATION NUMBER: US/09/462,917A  
 i CURRENT FILING DATE: 2000-04-03  
 i PRIORITY NUMBER: PCT/EP98/04522  
 i PRIOR FILING DATE: 1998-07-20  
 i NUMBER OF SEQ ID NOS: 152  
 i SOFTWARE: PatentIn version 3.0  
 i SEQ ID NO: 116  
 i LENGTH: 100  
 i TYPE: PRT  
 i ORGANISM: Human  
 us-09-462-917A-116

Query Match 84.0%; Score 220; DB 4; Length 100;  
 Best Local Similarity 85.1%; Pred. No. 7.4e-22;  
 Matches 40; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 MEQAPEDQGPAREPYNNEWTELLEELKSEAVRHFPRIWLHNGQHY 47  
 Db 1 MEQAPEDQGPAREPYNNEWTELLEELKSEAVRHFPRIWLHNGQHY 47

RESULT 15  
 us-09-462-917A-115  
 i Sequence 115, Application US/09462917A  
 i Patent No. 6511801  
 i GENERAL INFORMATION:  
 i APPLICANT: Delaporte, Eric  
 i APPLICANT: Peeters, Martine  
 i APPLICANT: Saman, Eric  
 i APPLICANT: Vanden Haesevelde, Marlen  
 i TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof  
 i FILE REFERENCE: INNS:014 11362\_0014.NPUS00  
 i CURRENT APPLICATION NUMBER: US/09/462,917A  
 i CURRENT FILING DATE: 2000-04-03  
 i PRIORITY NUMBER: PCT/EP98/04522  
 i PRIOR FILING DATE: 1998-07-20  
 i NUMBER OF SEQ ID NOS: 152  
 i SOFTWARE: PatentIn version 3.0  
 i SEQ ID NO: 115  
 i LENGTH: 100  
 i TYPE: PRT  
 i ORGANISM: Human  
 us-09-462-917A-115

Query Match 79.8%; Score 209; DB 4; Length 100;  
 Best Local Similarity 78.7%; Pred. No. 2.2e-20;  
 Matches 37; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 MEQAPEDQGPAREPYNNEWTELLEELKSEAVRHFPRIWLHNGQHY 47  
 Db 1 MERAPEDQGPAREPYNNEWTELLEELKSEAVRHFPRIWLHNGQHY 47

Search completed: October 18, 2004, 18:49:22  
 Job time : 28.4167 secs

Result	No.	Query	Score	Match	Length	DB	ID	Description
SUMMARIES								
-	1	262	100.0	96	14	US-10-059-261-272		Sequence 2/2, App
-	2	249	95.0	96	9	US-09-839-329-1		Sequence 1, Appl
-	3	248	94.7	78	14	US-10-283-618-15		Sequence 15, Appl
-	4	248	94.7	96	14	US-10-190-435-284		Sequence 284, App
-	5	244	93.1	96	14	US-10-190-435-276		Sequence 276, App
-	6	240	91.6	96	14	US-10-190-435-264		Sequence 264, App
-	7	240	91.6	96	14	US-10-190-435-265		Sequence 265, App
-	8	240	91.6	96	14	US-10-190-435-266		Sequence 266, App
-	9	240	91.6	96	14	US-10-190-435-282		Sequence 282, App
-	10	240	91.6	96	14	US-10-190-435-283		Sequence 283, App
-	11	240	91.6	96	15	US-10-296-734-4		Sequence 4, Appl
-	12	240	91.6	96	15	US-10-296-734-1475		Sequence 1475, App
-	13	239	91.2	96	14	US-10-190-435-258		Sequence 258, App
-	14	239	91.2	96	14	US-10-190-435-259		Sequence 259, App

i Publication No. US20020022027A1  
 i GENERAL INFORMATION:  
 i APPLICANT: Michael P. Sherman  
 i APPLICANT: Warner C. Greene  
 i APPLICANT: Carlos M.C. de No. 6664040chna  
 i APPLICANT: Ulrich Schubert  
 i APPLICANT: Peter Henklein  
 i TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF  
 i FILE REFERENCE: G&C 30448.91-US-02  
 i CURRENT APPLICATION NUMBER: US/09/8339,329  
 i PRIORITY FILING DATE: 2001-04-20  
 i PRIORITY APPLICATION NUMBER: 60/206,610  
 i PRIORITY FILING DATE: 2000-05-23  
 i PRIORITY APPLICATION NUMBER: 60/267,827  
 i NUMBER OF SEQ ID NOS: 5  
 i SOFTWARE: FastSEQ for Windows Version 4.0  
 i SEQ ID NO: 1  
 i LENGTH: 96  
 i TYPE: PRT  
 i ORGANISM: Artificial Sequence  
 i FEATURE: Synthetic Peptide of regulatory virus proteins R  
 i OTHER INFORMATION: (ypr) of human immunodeficiency virus type 1  
 i OTHER INFORMATION: (HIV-1)  
 i US-09-8339-329-1

Query Match 95.0%; Score 249; DB 9; Length 96;  
 Best Local Similarity 97.9%; Pred. No. 8.2e-23;  
 Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRITHLNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRITHLNLGQHIV 47

RESULT 3  
 US-10-283-618-15  
 i Sequence 15, Application US/10283618  
 i Publication No. US20030165517A1  
 i GENERAL INFORMATION:  
 i APPLICANT: Nicolette, Charles A.  
 i APPLICANT: Walker, Bruce  
 i TITLE OF INVENTION: THERAPEUTIC ANTI-HIV (ypr) COMPOUNDS  
 i FILE REFERENCE: GZ\_2111.00  
 i CURRENT APPLICATION NUMBER: US/10/283,618  
 i PRIORITY FILING DATE: 2002-10-29  
 i PRIORITY APPLICATION NUMBER: 60/345,957  
 i PRIORITY FILING DATE: 2001-10-29  
 i SOFTWARE: FastSEQ for Windows Version 4.0  
 i SEQ ID NO: 15  
 i LENGTH: 78  
 i TYPE: PRT  
 i ORGANISM: Human Immunodeficiency Virus  
 i US-10-283-618-15

Query Match 94.7%; Score 248; DB 14; Length 78;  
 Best Local Similarity 93.6%; Pred. No. 8.6e-23;  
 Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRITHLNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRITHLNLGQHIV 47

RESULT 4  
 US-10-190-435-284  
 i Sequence 284, Application US/10190435  
 i Publication No. US20030143248A1  
 i GENERAL INFORMATION:  
 i APPLICANT: ZUR MEGEDE, Jan

Query Match 94.7%; Score 248; DB 14; Length 96;  
 Best Local Similarity 93.6%; Pred. No. 1.1e-22;  
 Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRITHLNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRITHLNLGQHIV 47

RESULT 5  
 US-10-190-435-276  
 i Sequence 276, Application US/10190435  
 i Publication No. US20030143248A1  
 i GENERAL INFORMATION:  
 i APPLICANT: ZUR MEGEDE, Jan  
 i APPLICANT: BARNETT, Susan W.  
 i APPLICANT: LIAN, Ying  
 i APPLICANT: ENGELBRECHT, Susan  
 i APPLICANT: VAN RENSBURG, Estrelita J.  
 i TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF  
 i FILE REFERENCE: PP16133.003 / 2302-18133  
 i CURRENT APPLICATION NUMBER: US/10/190,435  
 i PRIORITY FILING DATE: 2002-12-30  
 i NUMBER OF SEQ ID NOS: 319  
 i SOFTWARE: PatentIn Ver. 2.0  
 i SEQ ID NO: 284  
 i LENGTH: 96  
 i TYPE: PRT  
 i ORGANISM: Artificial Sequence  
 i FEATURE:  
 i OTHER INFORMATION: Description of Artificial Sequence: Vpr HXB2  
 i US-10-190-435-284

Query Match 94.7%; Score 248; DB 14; Length 96;  
 Best Local Similarity 93.6%; Pred. No. 1.1e-22;  
 Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRITHLNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRITHLNLGQHIV 47

RESULT 6  
 US-10-190-435-276  
 i Sequence 276, Application US/10190435  
 i Publication No. US20030143248A1  
 i GENERAL INFORMATION:  
 i APPLICANT: ZUR MEGEDE, Jan  
 i APPLICANT: BARNETT, Susan W.  
 i APPLICANT: LIAN, Ying  
 i APPLICANT: ENGELBRECHT, Susan  
 i APPLICANT: VAN RENSBURG, Estrelita J.  
 i TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C

1 TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
 1 FILE REFERENCE: PP18133.003 / 2302-18133  
 1 CURRENT APPLICATION NUMBER: US/10/190,435  
 1 CURRENT FILING DATE: 2002-12-30  
 1 NUMBER OF SEQ ID NOS: 319  
 1 SOFTWARE: PatentIn Ver. 2.0  
 1 SEQ ID NO: 264  
 1 LENGTH: 96  
 1 TYPE: PRT  
 1 ORGANISM: Artificial Sequence  
 1 FEATURE: Artificial Sequence  
 1 OTHER INFORMATION: Description of Artificial Sequence: Vpr TV018-7  
 US-10-190-435-264

Qy 1 MEQAPEDQGPQREPYNNEWTLEELLELKSEAVRHFPRIWLNLGQHIV 47  
 Best Local Similarity 91.5%; Pred. No. 1e-21; Matches 43; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 MEQAPEDQGPQREPYNNEWTLEELLELKSEAVRHFPRIWLNLGQHIV 47

RESULT 7  
 US-10-190-435-265  
 Sequence 265, Application US/10190435  
 Publication No. US20030143248A1

GENERAL INFORMATION:  
 APPLICANT: ZUR MEGEDE, Jan  
 APPLICANT: BARNETT, Susan W.  
 APPLICANT: LIAN, Ying  
 APPLICANT: ENGELBRECHT, Susan  
 APPLICANT: VAN RENSBURG, Estrelita J.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
 FILE REFERENCE: PP18133.003 / 2302-18133  
 CURRENT APPLICATION NUMBER: US/10/190,435  
 CURRENT FILING DATE: 2002-12-30  
 NUMBER OF SEQ ID NOS: 319  
 SOFTWARE: PatentIn Ver. 2.0  
 LENGTH: 96  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Vpr TV018-8  
 US-10-190-435-265

Qy 1 MEQAPEDQGPQREPYNNEWTLEELLELKSEAVRHFPRIWLNLGQHIV 47  
 Best Local Similarity 91.5%; Pred. No. 1e-21; Matches 43; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 MEQAPEDQGPQREPYNNEWTLEELLELKSEAVRHFPRIWLNLGQHIV 47

RESULT 8  
 US-10-190-435-266  
 Sequence 266, Application US/10190435  
 Publication No. US20030143248A1

GENERAL INFORMATION:  
 APPLICANT: ZUR MEGEDE, Jan  
 APPLICANT: BARNETT, Susan W.  
 APPLICANT: LIAN, Ying  
 APPLICANT: ENGELBRECHT, Susan  
 APPLICANT: VAN RENSBURG, Estrelita J.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
 FILE REFERENCE: PP18133.003 / 2302-18133  
 CURRENT APPLICATION NUMBER: US/10/190,435  
 CURRENT FILING DATE: 2002-12-30  
 NUMBER OF SEQ ID NOS: 319  
 SOFTWARE: PatentIn Ver. 2.0  
 LENGTH: 96  
 TYPE: PRT  
 ORGANISM: Artificial Sequence

1 SOFTWARE: PatentIn Ver. 2.0  
 1 SEQ ID NO: 266  
 1 LENGTH: 96  
 1 TYPE: PRT  
 1 ORGANISM: Artificial Sequence  
 1 FEATURE:  
 1 OTHER INFORMATION: Description of Artificial Sequence: vpr TV002-84  
 US-10-190-435-266

Query Match 91.6%; Score 240; DB 14; Length 96;  
 Best Local Similarity 91.5%; Pred. No. 1e-21; Matches 43; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNNEWTLEELLELKSEAVRHFPRIWLNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELLELKSEAVRHFPRIWLNLGQHIV 47

RESULT 9  
 US-10-190-435-282  
 Sequence 282, Application US/10190435  
 Publication No. US20030143248A1

GENERAL INFORMATION:  
 APPLICANT: ZUR MEGEDE, Jan  
 APPLICANT: BARNETT, Susan W.  
 APPLICANT: LIAN, Ying  
 APPLICANT: ENGELBRECHT, Susan  
 APPLICANT: VAN RENSBURG, Estrelita J.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
 FILE REFERENCE: PP18133.003 / 2302-18133  
 CURRENT APPLICATION NUMBER: US/10/190,435  
 CURRENT FILING DATE: 2002-12-30  
 NUMBER OF SEQ ID NOS: 319  
 SOFTWARE: PatentIn Ver. 2.0  
 LENGTH: 96  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Vpr 96BM12-10  
 US-10-190-435-282

Query Match 91.6%; Score 240; DB 14; Length 96;  
 Best Local Similarity 91.5%; Pred. No. 1e-21; Matches 43; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEQAPEDQGPQREPYNNEWTLEELLELKSEAVRHFPRIWLNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELLELKSEAVRHFPRIWLNLGQHIV 47

RESULT 10  
 US-10-190-435-283  
 Sequence 283, Application US/10190435  
 Publication No. US20030143248A1

GENERAL INFORMATION:  
 APPLICANT: ZUR MEGEDE, Jan  
 APPLICANT: BARNETT, Susan W.  
 APPLICANT: LIAN, Ying  
 APPLICANT: ENGELBRECHT, Susan  
 APPLICANT: VAN RENSBURG, Estrelita J.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
 FILE REFERENCE: PP18133.003 / 2302-18133  
 CURRENT APPLICATION NUMBER: US/10/190,435  
 CURRENT FILING DATE: 2002-12-30  
 NUMBER OF SEQ ID NOS: 319  
 SOFTWARE: PatentIn Ver. 2.0  
 LENGTH: 96  
 TYPE: PRT  
 ORGANISM: Artificial Sequence

; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Vpr C2220-Bth  
 US-10-190-435-283

Query Match      91.6%;    Score 240;    DB 14;    Length 96;  
 Best Local Similarity    91.5%;    Pred. No. 1e-21;  
 Matches    43;    Conservative    1;    Mismatches    3;    Indels    0;    Gaps    0;

Qy    1 MEQAPEDQGPREPYNNEWTLEELKSEAVRHFPRIWLHNIGQHIV 47  
 Db    1 MEQAPEDQGPREPYNNEWAELLEELKQEAVRHFPRIWLHNIGQHIV 47

RESULT 11  
 US-10-296-734-4

; FILE REFERENCE: Application US/10396734  
 ; Publication No. US20040054137A1  
 ; GENERAL INFORMATION:  
 ;    APPLICANT: Thompson, Scott A  
 ;    TITLE OF INVENTION: Synthetic molecules and uses therefor  
 ;    FILE REFERENCE: Savine  
 ;    CURRENT APPLICATION NUMBER: US/10/296,734  
 ;    CURRENT FILING DATE: 2003-08-04  
 ;    PRIOR APPLICATION NUMBER: AU PQ7761/00  
 ;    PRIOR FILING DATE: 2000-05-26  
 ;    NUMBER OF SEQ ID NOS: 1507  
 ;    SOFTWARE: PatentIn Ver. 3.2  
 ;    SEQ ID NO 4  
 ;    LENGTH: 96  
 ;    TYPE: PRT  
 ;    ORGANISM: Artificial  
 ;    FEATURE:  
 ;    OTHER INFORMATION: VPR consensus polypeptide  
 ;    US-10-296-734-4

Query Match      91.6%;    Score 240;    DB 15;    Length 96;  
 Best Local Similarity    91.5%;    Pred. No. 1e-21;  
 Matches    43;    Conservative    1;    Mismatches    3;    Indels    0;    Gaps    0;

Qy    1 MEQAPEDQGPREPYNNEWTLEELKSEAVRHFPRIWLHNIGQHIV 47  
 Db    1 MEQAPEDQGPREPYNNEWAELLEELKQEAVRHFPRIWLHNIGQHIV 47

RESULT 12  
 US-10-296-734-4-1475

; Sequence 1475, Application US/10296734  
 ; Publication No. US20040054137A1  
 ; GENERAL INFORMATION:  
 ;    APPLICANT: Thompson, Scott A  
 ;    APPLICANT: Ramshaw, Ian A  
 ;    TITLE OF INVENTION: Synthetic molecules and uses therefor  
 ;    FILE REFERENCE: Savine  
 ;    CURRENT APPLICATION NUMBER: US/10/296,734  
 ;    CURRENT FILING DATE: 2003-08-04  
 ;    PRIOR APPLICATION NUMBER: AU PQ7761/00  
 ;    PRIOR FILING DATE: 2000-05-26  
 ;    NUMBER OF SEQ ID NOS: 1507  
 ;    SOFTWARE: PatentIn version 3.2  
 ;    SEQ ID NO 1475  
 ;    LENGTH: 96  
 ;    TYPE: PRT  
 ;    ORGANISM: Human immunodeficiency virus

Query Match      91.6%;    Score 240;    DB 15;    Length 96;  
 Best Local Similarity    91.5%;    Pred. No. 1e-21;  
 Matches    43;    Conservative    1;    Mismatches    3;    Indels    0;    Gaps    0;

Qy    1 MEQAPEDQGPREPYNNEWTLEELKSEAVRHFPRIWLHNIGQHIV 47  
 Db    1 MEQAPEDQGPREPYNNEWAELLEELKQEAVRHFPRIWLHNIGQHIV 47

RESULT 13  
 US-10-190-435-258

; Sequence 258, Application US/10190435  
 ; Publication No. US20030143248A1  
 ; GENERAL INFORMATION:  
 ;    APPLICANT: ZUR MEGDE, Jan  
 ;    APPLICANT: BARNETT, Susan W.  
 ;    APPLICANT: LIAN, Ying  
 ;    APPLICANT: ENGELBRECHT, Susan  
 ;    APPLICANT: VAN RENSBURG, Ettralita J.  
 ;    TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
 ;    FILE REFERENCE: PPI8133.003 / 2302-18133  
 ;    CURRENT APPLICATION NUMBER: US/10/190,435  
 ;    CURRENT FILING DATE: 2002-12-30  
 ;    NUMBER OF SEQ ID NOS: 319  
 ;    SOFTWARE: PatentIn Ver. 2.0  
 ;    SEQ ID NO 258  
 ;    LENGTH: 96  
 ;    TYPE: PRT  
 ;    ORGANISM: Artificial Sequence  
 ;    FEATURE:  
 ;    OTHER INFORMATION: Description of Artificial Sequence: Vpr TV008-17  
 ;    US-10-190-435-258

Query Match      91.2%;    Score 239;    DB 14;    Length 96;  
 Best Local Similarity    89.4%;    Pred. No. 1.e-21;  
 Matches    42;    Conservative    2;    Mismatches    3;    Indels    0;    Gaps    0;

Qy    1 MEQAPEDQGPREPYNNEWTLEELKSEAVRHFPRIWLHNIGQHIV 47  
 Db    1 MEQAPEDQGPREPYNNEWAELLEELKQEAVRHFPRIWLHNIGQHIV 47

RESULT 14  
 US-10-190-435-259

; Sequence 259, Application US/10190435  
 ; Publication No. US20030143248A1  
 ; GENERAL INFORMATION:  
 ;    APPLICANT: ZUR MEGDE, Jan  
 ;    APPLICANT: BARNETT, Susan W.  
 ;    APPLICANT: LIAN, Ying  
 ;    APPLICANT: ENGELBRECHT, Susan  
 ;    APPLICANT: VAN RENSBURG, Ettralita J.  
 ;    TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
 ;    FILE REFERENCE: PPI8133.003 / 2302-18133  
 ;    CURRENT APPLICATION NUMBER: US/10/190,435  
 ;    CURRENT FILING DATE: 2002-12-30  
 ;    NUMBER OF SEQ ID NOS: 319  
 ;    SOFTWARE: PatentIn Ver. 2.0  
 ;    SEQ ID NO 259  
 ;    LENGTH: 96  
 ;    TYPE: PRT  
 ;    ORGANISM: Artificial Sequence  
 ;    FEATURE:  
 ;    OTHER INFORMATION: Description of Artificial Sequence: Vpr TV008-1  
 ;    US-10-190-435-259

Query Match      91.2%;    Score 239;    DB 14;    Length 96;  
 Best Local Similarity    89.4%;    Pred. No. 1.e-21;  
 Matches    42;    Conservative    2;    Mismatches    3;    Indels    0;    Gaps    0;

Qy    1 MEQAPEDQGPREPYNNEWTLEELKSEAVRHFPRIWLHNIGQHIV 47  
 Db    1 MEQAPEDQGPREPYNNEWAELLEELKQEAVRHFPRIWLHNIGQHIV 47

RESULT 15  
 US-10-190-435-273

; Sequence 273, Application US/10190435

Publication No. US20030143248A1  
GENERAL INFORMATION:  
APPLICANT: BARNETT, Susan W.  
APPLICANT: LIAN, Ying  
APPLICANT: ENGELBRECHT, Susan  
APPLICANT: VAN RENSBURG, Estrelita J.  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF  
FILE REFERENCE: PP18133.003 / 2302-18133  
CURRENT APPLICATION NUMBER: US/10/190,435  
CURRENT FILING DATE: 2002-12-30  
NUMBER OF SEQ ID NOS: 319  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 273  
LENGTH: 96  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Vpr TV012-4  
US-10-190-435-73

Query Match 91.2%; Score 239; DB 14; Length 96;  
Best Local Similarity 89.4%; Pred. No. 1.4e-21;  
Matches 42; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MEQAPEDQGPOREPYNEWTGLEELKSEAVRHFPRIWLNLGQHIY 47  
Db 1 MEQAPEDQGPOREPYNEWTGLEELKSEAVRHFPRIWLNLGQHIY 47

Search completed: October 18, 2004, 18:52:22  
Job time : 85.1875 secs





Db 1 MERVPEPDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Superfamily: AIDS vpr protein

C;Keywords: AIDS; immunodeficiency

RESULT 3

T09444 vpr protein - human immunodeficiency virus type 1 (strain JRF1)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: T09444 R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, A; Reference number: Z16673

A;Accession: T09444 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-96 &lt;PAN&gt;

C;Cross-references: UNIPROT:Q75757; EMBL:U63632; NID:91465777; PID:91465784

C;Genetics:

A;Gene: vpr

C;Superfamily: AIDS vpr protein

RESULT 6

T01670 vpr protein - simian immunodeficiency virus SIVcpz

C;Species: simian immunodeficiency virus SIVcpz

C;Alternate names: orf-R protein

C;Note: host Pan troglodytes (chimpanzee)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004

R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.

Nature 345, 358-359, 1990

A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.

A;Reference number: S09983; PMID:90259077; PMID:2188136

A;Accession: S09986

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-96 &lt;HUE&gt;

A;Cross-references: UNIPROT:P17287; EMBL:X52154; NID:958866; PID:958870

C;Genetics:

A;Gene: vpr

C;Superfamily: AIDS vpr protein

C;Keywords: AIDS vpr protein

RESULT 7

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 09-Jul-2004

C;Accession: T01670 R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.

Cell 46, 63-74, 1986

A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol

A;Reference number: Z1389; PMID:86245056; PMID:2424612

A;Accession: T01670 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-96 &lt;ALI&gt;

A;Cross-references: UNIPROT:PO5955; EMBL:K03456; NID:960228; PID:960232

C;Superfamily: AIDS vpr protein

RESULT 8

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

C;Genetics:

RESULT 9

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

RESULT 10

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

RESULT 11

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

RESULT 12

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

RESULT 13

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

RESULT 14

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

RESULT 15

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

RESULT 16

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

RESULT 17

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

RESULT 18

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

RESULT 19

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

RESULT 20

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPVRWLHGLGQHIV 47

A;Gene: vpr

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: D44001 R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6517-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; PMID:93021387; PMID:1404605

A;Molecule type: DNA

A;Residues: 1-97 &lt;LIY&gt;

A;Cross-references: UNIPROT:P35967; GB:M93255

RESULT 21

vpr protein - simian immunodeficiency virus (macaque isolate)

N: Alternate names: orf R protein

C:Species: simian immunodeficiency virus, SIV

C:Accession: E28887 #sequence\_revision 30-Jun-1989 #text\_change 16-Jul-1999

R:Chakrabarti, L.; Guyader, M.; Alizon, M.; Daniel, M.D.; Desrosiers, R.C.; Tiollais, P.

Nature 328, 543-547, 1987

A:Title: Sequence of simian immunodeficiency virus from macaque and its relationship to

A:Reference number: A28887; MUID:87287230; PMID:364576

A:Accession: E28887

A:Molecule type: DNA

A:Residues: 1-101 <HTR>

A:Cross-references: GB:Y00277; GB:ML6403; NID:961730; PIDN:CAA68383.1; PID:961735

C:Genetics:

A:Gene: vpr

C:Superfamily: AIDS vpr protein

C:Keywords: AIDS; immunodeficiency

Query Match 56.5%; Score 148; DB 1; Length 101;

Best Local Similarity 59.6%; Pred. No. 5.7e-11;

Matches 28; Conservative 11; Mismatches 6; Indels 2; Gaps 2;

Qy 2 EQAPEDQGPQREPYNWELLEELKSEAVRHF-PRWLHNQHQHY 47

Db 3 ERPPEDAPQREPWDENVVLEELKEALKHFDPRL-LTALGNHY 48

RESULT 11

T11563

vpr protein - simian immunodeficiency virus SIVsm (strain E543)

C:Species: simian immunodeficiency virus SIVsm

A:Variety: strain E543

C:Accession: T11563 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

R:Hirsch, V.M.; Adger-Johnson, D.; Campbell, B.; Goldstein, S.; Brown, C.; Elkins, W.R.; N.

J. Virol. 71, 1608-1620, 1997

A:Title: A molecularly cloned, pathogenic, neutralization-resistant simian immunodeficiency virus

A:Reference number: 217285; MUID:97151152; PMID:8995688

A:Accession: T11563

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-101 <HTR>

A:Cross-references: UNIPROT:P89157; EMBL:U72748; NID:91695908; PIDN:AC56562.1; PID:91695908

C:Genetics:

A:Gene: vpr

C:Superfamily: AIDS vpr protein

C:Keywords: AIDS; immunodeficiency

Query Match 54.6%; Score 143; DB 2; Length 101;

Best Local Similarity 57.4%; Pred. No. 2.3e-10;

Matches 27; Conservative 11; Mismatches 7; Indels 2; Gaps 2;

Qy 2 EQAPEDQGPQREPYNWELLEELKSEAVRHF-PRWLHNQHQHY 47

Db 3 ERPPEDAPQREPWDENVVLEELKEALKHFDPRL-LTALGNHY 48

RESULT 12

S28083

vpr protein - simian immunodeficiency virus

C:Species: simian immunodeficiency virus SIV

C:Accession: E26737 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004

R:Hirsch, V.; Riedel, N.; Mullins, J.I.

Cell 49, 307-319, 1987

A:Title: The genome organization of STLV-3 is similar to that of the AIDS virus except for

A:Reference number: A26737; MUID:87187627; PMID:3646094

A:Accession: E26737

A:Molecule type: DNA

A:Residues: 1-122 <HTR>

A:Cross-references: UNIPROT:P11265; GB:MI9499; NID:9334657

C:Genetics:

A:Gene: vpr

C:Superfamily: AIDS vpr protein

C:Keywords: AIDS; immunodeficiency

Query Match 56.3%; Score 147.5; DB 1; Length 122;

Best Local Similarity 61.2%; Pred. No. 8.1e-11;

Matches 30; Conservative 10; Mismatches 6; Indels 3; Gaps 3;

Qy 1 MEQAP-EDGPQREPYNWELLEELKSEAVRHF-PRWLHNQHQHY 47

Db 1 MEERPLENGQREPWDENVVLEELKEALKHFDPRL-LTALGNHY 48

RESULT 10

S07991

vpr protein - simian immunodeficiency virus SIVsm (isolate F236)

C:Species: simian immunodeficiency virus SIVsm

C:Accession: S07991 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

R:Hirsch, V.M.; Olmsted, R.A.; Murphy-Corb, M.; Purcell, R.H.; Johnson, P.R.

Nature 339, 389-392, 1989

A:Title: An African primate lentivirus (SIV<sup>sm</sup>) closely related to HIV-2.

A:Reference number: S04237; MUID:8922053; PMID:2786147

A:Accession: S07991

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: genomic RNA

A:Residues: 1-89 <HTR>

A:Cross-references: UNIPROT:P12521; EMBL:X14307; NID:961741; PIDN:CAA32486.1; PID:961745

A:Note: this sequence was submitted to the EMBL Data Library, February 1989

RESULT 13

553095 vpr protein - human immunodeficiency virus type 2  
 C;Species: human immunodeficiency virus type 2, HIV-2  
 C;Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
 R;Becker, M.; Zorr, B.; Becker, A.; Habermehl, K.O.  
 Submitted to the EMBL Data Library, March 1995  
 A;Description: Molecular and phylogenetic characterisation of a Guinea-Bissau-derived hu  
 A;Reference number: S53091  
 A;Accession: S53095  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-105 <BEC>  
 A;Cross-references: UNIPROT:Q76624; EMBL:248731; NID:9732718; PIDN:CPA88624.1; PID:973271  
 C;Superfamily: AIDS vpr protein

Query Match 48.9% Score 128; DB 2; Length 105;  
 Best Local Similarity 52.9%; Pred. No. 1.6e-08;  
 Matches 24; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 2 EQAPEDQGPQREPYNWELLEELKSEAVRHF-PRIWNLGQHRY 47  
 Db 7 ELPEDGTPPREPGDENVIEILREITEALKHFDRSLLTALGRHY 52

RESULT 14

508439 vpr protein - human immunodeficiency virus type 2 D205  
 C;Species: human immunodeficiency virus type 2 D205  
 C;Date: 07-Sep-1990 #sequence\_revision 07-spp-1990 #text\_change 09-Jul-2004  
 R;Dietrich, U.; Adamski, M.; Kreutz, R.; Seipp, A.; Kuehnel, H.; Ruebsamen-Waigmann, H.  
 A;Title: A highly divergent HIV-2-related isolate.  
 A;Reference number: S08439  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-101 <DIE>  
 A;Cross-references: UNIPROT:PI15837; EMBL:X16109  
 A;Note: this sequence was submitted to the EMBL Data Library, Aug-1989  
 C;Genetics:  
 A;Gene: vpr  
 C;Superfamily: AIDS vpr protein

Query Match 47.7% Score 125; DB 2; Length 101;  
 Best Local Similarity 55.3%; Pred. No. 3.6e-08;  
 Matches 26; Conservative 8; Mismatches 11; Indels 2; Gaps 2;

Qy 2 EQAPEDQGPQREPYNWELLEELKSEAVRHF-PRIWNLGQHRY 47  
 Db 7 EIPPEENNQREPEWENNGEELIEKQALKHFDPNU-LTALGRHY 52

RESULT 15

508439 vpr protein - human immunodeficiency virus type 2 (isolate CAM2/Guinea-Bissau)  
 C;Alternate names: orf-R protein  
 C;Species: human immunodeficiency virus type 2, HIV-2  
 A;Note: host Homo sapiens (man)  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C;Accession: E38475; JQ09775  
 R;Tristem, M.; Hill, F.; Karpas, A.  
 A;Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus type  
 A;Reference number: A38475; MUID:9117059; PMID:2005437  
 A;Molecule type: DNA  
 A;Residues: 1-104 <TRI>  
 A;Cross-references: UNIPROT:P24111; GB:D00835; NID:93153166; PIDN:BAA00713.1; PID:922147  
 C;Genetics:  
 A;Gene: vpr  
 C;Superfamily: AIDS vpr protein



DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Vpr protein.  
 GN Name=vpr;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1] \_  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21268728; PubMed=11375060;  
 RA Halani N., Wang B., Ge Y.C., Gharpure H., Hira S., Saksena N.K.;  
 RA "Changing epidemiology of HIV type 1 infections in India: evidence of  
 RT subtype B introduction in Bombay from a common source.";  
 RT AIDS Res. Hum. Retroviruses 17:637-642 (2001).  
 RL AIDS Res. Hum. Retroviruses 17:637-642 (2001).  
 DR EMBL; AF316100; AAC11288.1; -.  
 DR HSSP; P12520; 1DSJ.  
 DR InterPro; IPR000012; Retrov\_Vpr/X.  
 DR Pfam; PF00522; VPR; 1.  
 DR PRINTS; PR00444; HIVPRVX.  
 DR AIDS.  
 KW AIDS.  
 SQ SEQUENCE 96 AA; 11377 MW; 58BC5358EB286D4F CRC64;  
 Query Match 100.0%; Score 262; DB 2; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-24;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;  
 Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47

## RESULT 3

Q99DD7 PRELIMINARY; PRT; 96 AA.  
 ID Q99DD7; PRELIMINARY;  
 AC 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Vpr protein.  
 GN Name=vpr;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1] \_  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21268767; PubMed=11375060;  
 RA Halani N., Wang B., Ge Y.C., Gharpure H., Hira S., Saksena N.K.;  
 RA "Changing epidemiology of HIV type 1 infections in India: evidence of  
 RT subtype B introduction in Bombay from a common source.";  
 RT AIDS Res. Hum. Retroviruses 17:637-642 (2001).  
 RL AIDS Res. Hum. Retroviruses 17:637-642 (2001).  
 DR EMBL; AF316100; AAC11288.1; -.  
 DR HSSP; P12520; 1DSJ.  
 DR InterPro; IPR000012; Retrov\_Vpr/X.  
 DR Pfam; PF00522; VPR; 1.  
 DR PRINTS; PR00444; HIVPRVX.  
 DR AIDS.  
 SQ SEQUENCE 96 AA; 11377 MW; 58BC5358EB286D4F CRC64;

Query Match 99.6%; Score 261; DB 2; Length 96;  
 Best Local Similarity 97.9%; Pred. No. 1.7e-24;  
 Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Gaps 0;  
 Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47

## RESULT 4

Q99DD8 PRELIMINARY; PRT; 96 AA.  
 ID Q99DD8; PRELIMINARY;  
 AC 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DR 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Vpr protein.  
 GN Name=vpr;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1] \_  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21268767; PubMed=11375060;  
 RA Halani N., Wang B., Ge Y.C., Gharpure H., Hira S., Saksena N.K.;  
 RA "Changing epidemiology of HIV type 1 infections in India: evidence of  
 RT subtype B introduction in Bombay from a common source.";  
 RT AIDS Res. Hum. Retroviruses 17:637-642 (2001).  
 RL AIDS Res. Hum. Retroviruses 17:637-642 (2001).  
 DR EMBL; AF316100; AAC11288.1; -.  
 DR HSSP; P12520; 1DSJ.  
 DR InterPro; IPR000012; Retrov\_Vpr/X.  
 DR Pfam; PF00522; VPR; 1.  
 DR PRINTS; PR00444; HIVPRVX.  
 DR AIDS.  
 KW AIDS.  
 SQ SEQUENCE 96 AA; 11363 MW; 58BC534A5CD86D4F CRC64;  
 Query Match 99.6%; Score 261; DB 2; Length 96;  
 Best Local Similarity 97.9%; Pred. No. 1.7e-24;  
 Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Gaps 0;  
 Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47

## RESULT 5

Q99601 PRELIMINARY; PRT; 96 AA.  
 ID Q99601; PRELIMINARY;  
 AC 089601; PRELIMINARY;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Vpr Protein (Fragment).  
 GN Name=vpr;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1] \_  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2832522; PubMed=9658150;  
 RA Yedavalli V.R., Chappay C., Ahmed N.;  
 RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene  
 following mother-to-infant transmission.";  
 RL J. Virol. 72:6937-6943 (1998).  
 DR EMBL; AF042911; AAC41078.1; -.  
 DR InterPro; IPR000012; Retrov\_Vpr/X.  
 DR Pfam; PF00522; VPR; 1.  
 DR PRINTS; PR00444; HIVPRVX.  
 DR AIDS.  
 FT NON TER  
 SQ SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241\_CRC64;

Query Match 98.9%; Score 259; DB 2; Length 96;  
 Best Local Similarity 97.9%; Pred. No. 2.9e-24;  
 Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Gaps 0;  
 Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47  
 Db 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47

## RESULT 6

Q99602 PRELIMINARY; PRT; 96 AA.  
 ID Q99602; PRELIMINARY;  
 AC 089602; PRELIMINARY;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE	Vpr protein (Fragment).
GN	Name=vpr
OS	Human immunodeficiency virus 1.
OC	Viruses; Retroviridae; Lentiviridae; Lentivirus.
OX	NCBI_TaxID:11676;
RN	
RP	SEQUENCE FROM N.A. MEDLINE:98325222; PubMed=9655150;
RX	Yedavalli V.R., Chappay C., Ahmad N.; "Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission."; J. Virol. 72:6937-6943 (1998).
RA	EMBL; AF042912; AAC41000.1; InterPro; IPR000012; Retrov_vpr/X.
RT	InterPro; IPR000012; Retrov_vpr/X.
RT	PFAM; PF00522; VPR; 1.
RT	PRINTS; PR00444; HIVPRVpx.
RT	AIDS.
KW	
FT	NON TER 96 96 AA; 11416 MW; DB954C0F2C808241 CRC64;
SQ	SEQUENCE 96 AA; 11416 MW; DB95484EC4877220 CRC64;
Query Match	Score 259; DB 2; Length 96;
Best Local Similarity	98.9%;
Matches	Pred. No. 2.9e-24;
Qy	1 MEQAPEDQGPQREPYNNEWTLEELLELKSBAVRHPPRIMLNLGQHY 47
Db	1 MEQAPEDQGPQREPYNNEWTLEELLELKSBAVRHPPRIMLNLGQHY 47
RESULT 7	089603
RP	SEQUENCE FROM N.A. MEDLINE:98325222; PubMed=9655150;
ID	089603; PRELIMINARY; PRT; 96 AA.
AC	089603; (TREMBLrel. 08, Created)
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 08, Last annotation update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Vpr protein (Fragment).
DE	Name=vpr;
GN	Human immunodeficiency virus 1.
OS	Human immunodeficiency virus 1.
OC	Viruses; Retroviridae; Lentiviridae; Lentivirus.
OX	NCBI_TaxID:11676;
RN	
RP	SEQUENCE FROM N.A. MEDLINE:98325222; PubMed=9655150;
RX	Yedavalli V.R., Chappay C., Ahmad N.; "Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission."; J. Virol. 72:6937-6943 (1998).
RA	EMBL; AF042912; AAC41000.1; InterPro; IPR000012; Retrov_vpr/X.
RT	InterPro; IPR000012; Retrov_vpr/X.
RT	PFAM; PF00522; VPR; 1.
RT	PRINTS; PR00444; HIVPRVpx.
RT	AIDS.
FT	NON TER 96 96 AA; 11446 MW; DB9552FEC3808241 CRC64;
SQ	SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;
Query Match	Score 259; DB 2; Length 96;
Best Local Similarity	98.9%;
Matches	Pred. No. 2.9e-24;
Qy	1 MEQAPEDQGPQREPYNNEWTLEELLELKSBAVRHPPRIMLNLGQHY 47
Db	1 MEQAPEDQGPQREPYNNEWTLEELLELKSBAVRHPPRIMLNLGQHY 47
RESULT 8	089604
RP	SEQUENCE FROM N.A. MEDLINE:98325222; PubMed=9655150;
ID	089604; PRELIMINARY; PRT; 96 AA.
AC	089604; (TREMBLrel. 08, Created)
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	Vpr protein (Fragment).
DE	Name=vpr;
GN	Human immunodeficiency virus 1.
OS	Human immunodeficiency virus 1.
OC	Viruses; Retroviridae; Lentiviridae; Lentivirus.
OX	NCBI_TaxID:11676;
RN	
RP	SEQUENCE FROM N.A. MEDLINE:98325222; PubMed=9655150;
RX	Yedavalli V.R., Chappay C., Ahmad N.; "Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission."; J. Virol. 72:6937-6943 (1998).
RA	EMBL; AF042912; AAC41000.1; InterPro; IPR000012; Retrov_vpr/X.
RT	InterPro; IPR000012; Retrov_vpr/X.
RT	PFAM; PF00522; VPR; 1.
RT	PRINTS; PR00444; HIVPRVpx.
RT	AIDS.
FT	NON TER 96 96 AA; 11446 MW; DB9552FEC3808241 CRC64;
SQ	SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;
Query Match	Score 259; DB 2; Length 96;
Best Local Similarity	98.9%;
Matches	Pred. No. 2.9e-24;
Qy	1 MEQAPEDQGPQREPYNNEWTLEELLELKSBAVRHPPRIMLNLGQHY 47
Db	1 MEQAPEDQGPQREPYNNEWTLEELLELKSBAVRHPPRIMLNLGQHY 47
RESULT 9	089606
RP	SEQUENCE FROM N.A. MEDLINE:98325222; PubMed=9655150;
ID	089606; PRELIMINARY; PRT; 96 AA.
AC	089606; (TREMBLrel. 08, Created)
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Vpr protein (Fragment).
DE	Name=vpr;
GN	Human immunodeficiency virus 1.
OS	Human immunodeficiency virus 1.
OC	Viruses; Retroviridae; Lentiviridae; Lentivirus.
OX	NCBI_TaxID:11676;
RN	
RP	SEQUENCE FROM N.A. MEDLINE:98325222; PubMed=9655150;
RX	Yedavalli V.R., Chappay C., Ahmad N.; "Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission."; J. Virol. 72:6937-6943 (1998).
RA	EMBL; AF042912; AAC41000.1; InterPro; IPR000012; Retrov_vpr/X.
RT	InterPro; IPR000012; Retrov_vpr/X.
RT	PFAM; PF00522; VPR; 1.
RT	PRINTS; PR00444; HIVPRVpx.
RT	AIDS.
FT	NON TER 96 96 AA; 11446 MW; DB9552FEC3808241 CRC64;
SQ	SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;
Query Match	Score 259; DB 2; Length 96;
Best Local Similarity	98.9%;
Matches	Pred. No. 2.9e-24;
Qy	1 MEQAPEDQGPQREPYNNEWTLEELLELKSBAVRHPPRIMLNLGQHY 47
Db	1 MEQAPEDQGPQREPYNNEWTLEELLELKSBAVRHPPRIMLNLGQHY 47
RESULT 10	089608
RP	SEQUENCE FROM N.A. MEDLINE:98325222; PubMed=9655150;
ID	089608; PRELIMINARY; PRT; 96 AA.
AC	089608; (TREMBLrel. 08, Created)
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Vpr protein (Fragment).
DE	Name=vpr;
GN	Human immunodeficiency virus 1.
OS	Human immunodeficiency virus 1.
OC	Viruses; Retroviridae; Lentiviridae; Lentivirus.
OX	NCBI_TaxID:11676;
RN	
RP	SEQUENCE FROM N.A. MEDLINE:98325222; PubMed=9655150;
RX	Yedavalli V.R., Chappay C., Ahmad N.; "Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission."; J. Virol. 72:6937-6943 (1998).
RA	EMBL; AF042912; AAC41000.1; InterPro; IPR000012; Retrov_vpr/X.
RT	InterPro; IPR000012; Retrov_vpr/X.
RT	PFAM; PF00522; VPR; 1.
RT	PRINTS; PR00444; HIVPRVpx.
RT	AIDS.
FT	NON TER 96 96 AA; 11446 MW; DB9552FEC3808241 CRC64;
SQ	SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;
Query Match	Score 259; DB 2; Length 96;
Best Local Similarity	98.9%;
Matches	Pred. No. 2.9e-24;
Qy	1 MEQAPEDQGPQREPYNNEWTLEELLELKSBAVRHPPRIMLNLGQHY 47
Db	1 MEQAPEDQGPQREPYNNEWTLEELLELKSBAVRHPPRIMLNLGQHY 47

OC	Viruses; Retroviruses; Retroviridae; Lentivirus.	OX	NCBI_TaxID=11676;
RN	[1] _TaxID=11676;	RN	NCBI_TaxID=11676;
RP	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RX	Medline=9832522; PubMed=9658150;	RX	Medline=9832522; PubMed=9658150;
RA	Yedavalli V.R., Chappay C., Ahmad N.;	RA	Yedavalli V.R., Chappay C., Ahmad N.;
RT	"Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission.";	RT	"Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission.";
RT	J. Virol. 72:6937-6943(1998).	RT	J. Virol. 72:6937-6943(1998).
RL	EMBL; AF042919; AAC41085.1;	DR	EMBL; AF042921; AAC41087.1;
DR	InterPro; IPR00012; Retrov_Vpr/X.	DR	InterPro; IPR00012; Retrov_Vpr/X.
DR	Pfam; PF00522; VPR; 1.	DR	Pfam; PF00522; VPR; 1.
PRINTS;	PR00444; HIVPRVXP.	PRINTS;	PR00444; HIVPRVXP.
KW	AIDS.	KW	AIDS.
FT	NON_TER 96 96 AA; 11446 MW;	FT	NON_TER 96 96 AA; 11446 MW;
SQ	DB9552FEC3808241 CRC64;	SQ	DB9552FEC3808241 CRC64;
Query Match	Score 98.9%; Best Local Similarity 97.9%; Matches 46;	Query Match	Score 98.9%; Best Local Similarity 97.9%; Matches 46;
Qy	1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47	Qy	1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47
Db	1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47	Db	1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47
RESULT 11		RESULT 13	
089609	SEQUENCE FROM N.A.	089611	SEQUENCE FROM N.A.
ID	089609	ID	089611
AC	089609;	AC	089611;
DT	01-NOV-1998 (TREMBLrel. 08. Created)	DT	01-NOV-1998 (TREMBLrel. 08. Created)
DT	01-NOV-1998 (TREMBLrel. 08. Last sequence update)	DT	01-NOV-1998 (TREMBLrel. 08. Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24. Last annotation update)	DT	01-JUN-2003 (TREMBLrel. 24. Last annotation update)
DB	Vpr protein (Fragment).	DB	Vpr Protein (Fragment).
GN	Name=vpr;	GN	Name=vpr;
NA	Human immunodeficiency virus 1.	OS	Human immunodeficiency virus 1.
OC	Viruses; Retroviruses; Retroviridae; Lentivirus.	OC	Viruses; Retroviruses; Retroviridae; Lentivirus.
RN	[1] _TaxID=11676;	RN	NCBI_TaxID=11676;
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RX	Medline=9832522; PubMed=9658150;	RX	Medline=9832522; PubMed=9658150;
RA	Yedavalli V.R., Chappay C., Ahmad N.;	RA	Yedavalli V.R., Chappay C., Ahmad N.;
RT	"Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission.";	RT	"Maintenance of an intact human immunodeficiency virus type 1 vpr gene following mother-to-infant transmission.";
RT	J. Virol. 72:6937-6943(1998).	RT	J. Virol. 72:6937-6943(1998).
RL	EMBL; AF042920; AAC41086.1;	DR	EMBL; AF042922; AAC41088.1;
DR	InterPro; IPR00012; Retrov_Vpr/X.	DR	InterPro; IPR00012; Retrov_Vpr/X.
DR	Pfam; PF00522; VPR; 1.	DR	Pfam; PF00522; VPR; 1.
PRINTS;	PR00444; HIVPRVXP.	PRINTS;	PR00444; HIVPRVXP.
KW	AIDS.	KW	AIDS.
FT	NON_TER 96 96 AA; 11446 MW;	FT	NON_TER 96 96 AA; 11446 MW;
SQ	DB9552FEC3808241 CRC64;	SQ	DB9552FEC3808241 CRC64;
Query Match	Score 98.9%; Best Local Similarity 97.9%; Matches 46;	Query Match	Score 98.9%; Best Local Similarity 97.9%; Matches 46;
Qy	1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47	Qy	1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47
Db	1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47	Db	1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHFPRIWLNLGQHIV 47
RESULT 12		RESULT 14	
089610	SEQUENCE FROM N.A.	089612	SEQUENCE FROM N.A.
ID	089610	ID	089612
AC	089610;	AC	089612;
DT	01-NOV-1998 (TREMBLrel. 08. Created)	DT	01-NOV-1998 (TREMBLrel. 08. Created)
DT	01-NOV-1998 (TREMBLrel. 08. Last sequence update)	DT	01-NOV-1998 (TREMBLrel. 08. Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24. Last annotation update)	DT	01-OCT-2003 (TREMBLrel. 25. Last annotation update)
DB	Vpr protein (Fragment).	DB	Vpr Protein (Fragment).
GN	Name=vpr;	GN	Name=vpr;
NA	Human immunodeficiency virus 1.	OS	Human immunodeficiency virus 1.
OC	Viruses; Retroviruses; Retroviridae; Lentivirus.	OC	Viruses; Retroviruses; Retroviridae; Lentivirus.
RN	[1] _TaxID=11676;	RN	NCBI_TaxID=11676;

[1]

RN SEQUENCE FROM N.A.  
RP MEDLINE=98325222; PubMed=9658150;  
RX Yedavalli V.R., Chappay C., Ahmad N.;  
RT "Maintenance of an intact human immunodeficiency virus type 1 vpr gene  
following mother-to-infant transmission.";  
RL J. Virol. 72:5937-5943 (1998).  
DR EMBL; AF042923; AAC1089.1;  
InterPro; IPR000012; Retrov\_VPR/X.  
DR Pfam; PF00522; VPR; 1.  
PRINTS; PR00444; HIVPRVX.  
AIDS.  
FT NON TER 96 96  
SEQUENCE 96 AA; 11446 MW; DB9552FEC3808241 CRC64;  
SQ

---

RESULT 15

089613 PRELIMINARY; PRT; 96 AA.  
ID 089613  
AC 089613;  
Query Match 98.9%; Score 259; DB 2; Length 96;  
Best Local Similarity 97.9%; Pred. No. 2.9e-24;  
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRIWLNQHIY 47  
1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRIWLNQHIY 47

089613 PRELIMINARY; PRT; 96 AA.  
ID 089613  
AC 089613;  
Query Match 98.9%; Score 259; DB 2; Length 96;  
Best Local Similarity 97.9%; Pred. No. 2.9e-24;  
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRIWLNQHIY 47  
1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRIWLNQHIY 47

RESULT 16

089613 PRELIMINARY; PRT; 96 AA.  
ID 089613  
AC 089613;  
Query Match 98.9%; Score 259; DB 2; Length 96;  
Best Local Similarity 97.9%; Pred. No. 2.9e-24;  
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRIWLNQHIY 47  
1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRIWLNQHIY 47

089613 PRELIMINARY; PRT; 96 AA.  
ID 089613  
AC 089613;  
Query Match 98.9%; Score 259; DB 2; Length 96;  
Best Local Similarity 97.9%; Pred. No. 2.9e-24;  
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db

Qy 1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRIWLNQHIY 47  
1 MEQAPEDQGPQREPYNNEWTLEELKSEAVRHPRIWLNQHIY 47

Search completed: October 18, 2004, 18:47:36  
Job time : 59.75 sec8



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2004, 18:31:42 ; Search time 64.3125 Seconds  
(without alignments)

Title: US-09-913-927D-3  
Perfect score: 254  
Sequence: 1 ETYGDWTAGVBAIRILQQL.....RHSRIGVTRORRNGASRS 49

Scoring table: BLOSUM62  
Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$  
Listing first 45 summaries

Database : A\_GenSeq\_23Sep04:\*

1: genSeqD1980s:\*

2: genSeqD1990s:\*

3: genSeqD2000s:\*

4: genSeqD2001s:\*

5: genSeqD2002s:\*

6: genSeqD2003s:\*

7: genSeqD2003s:\*

8: genSeqD2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	254	100.0	49	AAB10687	Aab10687 HIV-1 reg
2	254	100.0	96	AAR48963	Aar48963 HIV VPR
3	254	100.0	96	AAW51040	Aaw51040 HIV-1 pol
4	254	100.0	96	AAB10049	Aab10049 HIV-1 vpr
5	254	100.0	96	AAB10685	Aab10685 HIV-1 reg
6	254	100.0	96	AAE16129	Aae16129 Human imm
7	254	100.0	96	ABP56175	ABP56175 HIV-1 vir
8	254	100.0	96	AAB80187	Aab80187 HIV-1 vpr
9	254	100.0	96	ADD01277	ADD01277 HIV-1 vpr
10	254	100.0	96	ADP16812	Adf16812 HIV-1 vpr
11	254	100.0	96	ABM79669	Abm79669 HIV-1 vpr
12	253	99.6	96	ADP20070	Adp20070 Human imm
13	250	98.4	95	ADP81477	Adp81477 HIV-1 vpr
14	250	98.4	96	AAR84544	Aar84544 Native Vp
15	250	98.4	96	AAY53247	Aay53247 HIV-1 LAI
16	249	98.0	96	ABR55491	Abf55491 Amino aci
17	249	98.0	96	ADP20078	Adp20078 Human imm
18	244	96.1	96	AAB63306	Aab63306 HIV-1 non
19	243	95.7	3032	ADP81468	Adp81468 Lymphaden
20	243	95.7	3033	ADA19379	Ada19379 Lymphaden
21	242	95.3	96	AAR10175	Aar10175 Rap (R) P
22	241	94.9	96	AAR12258	Aar12258 HIV-1 str
23	238	93.7	96	AAB63304	Aab63304 HIV-1 non
24	238	93.7	96	AAB63308	Aab63308 HIV-1 non
25	236	92.9	96	AAP81856	Aap81856 Sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	254	100.0	49	AAB10687	Aab10687 HIV-1 reg
2	254	100.0	96	AAR48963	Aar48963 HIV VPR
3	254	100.0	96	AAW51040	Aaw51040 HIV-1 pol
4	254	100.0	96	AAB10049	Aab10049 HIV-1 vpr
5	254	100.0	96	AAB10685	Aab10685 HIV-1 reg
6	254	100.0	96	AAE16129	Aae16129 Human imm
7	254	100.0	96	ABP56175	ABP56175 HIV-1 vir
8	254	100.0	96	AAB80187	Aab80187 HIV-1 vpr
9	254	100.0	96	ADD01277	ADD01277 HIV-1 vpr
10	254	100.0	96	ADP16812	Adf16812 HIV-1 vpr
11	254	100.0	96	ABM79669	Abm79669 HIV-1 vpr
12	253	99.6	96	ADP20070	Adp20070 Human imm
13	250	98.4	95	ADP81477	Adp81477 HIV-1 vpr
14	250	98.4	96	AAR84544	Aar84544 Native Vp
15	250	98.4	96	AAY53247	Aay53247 HIV-1 LAI
16	249	98.0	96	ABR55491	Abf55491 Amino aci
17	249	98.0	96	ADP20078	Adp20078 Human imm
18	244	96.1	96	AAB63306	Aab63306 HIV-1 non
19	243	95.7	3032	ADP81468	Adp81468 Lymphaden
20	243	95.7	3033	ADA19379	Ada19379 Lymphaden
21	242	95.3	96	AAR10175	Aar10175 Rap (R) P
22	241	94.9	96	AAR12258	Aar12258 HIV-1 str
23	238	93.7	96	AAB63304	Aab63304 HIV-1 non
24	238	93.7	96	AAB63308	Aab63308 HIV-1 non
25	236	92.9	96	AAP81856	Aap81856 Sequence

PS Claim 3.3; Page 5; 35PP; German.

XX This invention describes novel synthetic peptides (I) derived from the regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-1) which have antiviral activity and can be used for gene therapy. (I) is used for therapeutic and/or diagnostic purposes, especially in biological assays, for development of serological tests or enzyme-linked immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in blood), to raise specific antibodies and antisera (especially those reactive with specific epitopes), and as antiviral agents. (I) can also be used in screening for potential Vpr antagonists (i.e. compounds that

Result No.	Score	Query Match	Length	DB ID	Description
1	254	100.0	49	AAB10687	Aab10687 HIV-1 reg
2	254	100.0	96	AAR48963	Aar48963 HIV VPR
3	254	100.0	96	AAW51040	Aaw51040 HIV-1 pol
4	254	100.0	96	AAB10049	Aab10049 HIV-1 vpr
5	254	100.0	96	AAB10685	Aab10685 HIV-1 reg
6	254	100.0	96	AAE16129	Aae16129 Human imm
7	254	100.0	96	ABP56175	ABP56175 HIV-1 vir
8	254	100.0	96	AAB80187	Aab80187 HIV-1 vpr
9	254	100.0	96	ADD01277	ADD01277 HIV-1 vpr
10	254	100.0	96	ADP16812	Adf16812 HIV-1 vpr
11	254	100.0	96	ABM79669	Abm79669 HIV-1 vpr
12	253	99.6	96	ADP20070	Adp20070 Human imm
13	250	98.4	95	ADP81477	Adp81477 HIV-1 vpr
14	250	98.4	96	AAR84544	Aar84544 Native Vp
15	250	98.4	96	AAY53247	Aay53247 HIV-1 LAI
16	249	98.0	96	ABR55491	Abf55491 Amino aci
17	249	98.0	96	ADP20078	Adp20078 Human imm
18	244	96.1	96	AAB63306	Aab63306 HIV-1 non
19	243	95.7	3032	ADP81468	Adp81468 Lymphaden
20	243	95.7	3033	ADA19379	Ada19379 Lymphaden
21	242	95.3	96	AAR10175	Aar10175 Rap (R) P
22	241	94.9	96	AAR12258	Aar12258 HIV-1 str
23	238	93.7	96	AAB63304	Aab63304 HIV-1 non
24	238	93.7	96	AAB63308	Aab63308 HIV-1 non
25	236	92.9	96	AAP81856	Aap81856 Sequence

#### ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	254	100.0	49	AAB10687	Aab10687 standard, peptide, 49 AA.
2	254	100.0	96	AC	AC
3	254	100.0	96	XX	XX
4	254	100.0	96	DT	19-JAN-2001 (first entry)
5	254	100.0	96	XX	HIV-1 regulatory virus protein R peptide svpr8-96.
6	254	100.0	96	DE	Regulatory virus protein R: Vpr; antiviral; gene therapy; pathogenicity;
7	254	100.0	96	XX	Regulatory virus protein R: Vpr; antiviral; gene therapy; cell cycle arrest.
8	254	100.0	96	OS	Synthetic.
9	254	100.0	96	OS	Human immunodeficiency virus 1.
10	254	100.0	96	XX	OS
11	254	100.0	96	PN	PN
12	253	99.6	96	PD	WO20049038-A2.
13	250	98.4	95	PD	24-AUG-2000.
14	250	98.4	96	XX	XX
15	250	98.4	96	PP	19-FEB-2000; 2000WO-DE000325.
16	249	98.0	96	XX	XX
17	249	98.0	96	PR	19-FEB-1999; 99DE-01008752.
18	244	96.1	96	PR	19-FEB-1999; 99DE-01008766.
19	243	95.7	3032	PA	(SCHU/ ) SCHUBERT U.
20	243	95.7	3033	PA	(HENK/ ) HENKLEIN P.
21	242	95.3	96	XX	(WRAY/ ) WRAY V.
22	241	94.9	96	PI	Schubert U, Henklein P, Wray V;
23	238	93.7	96	XX	DR WPI; 2000-565367/52.
24	238	93.7	96	PT	New synthetic peptides from the Vpr protein of human immune deficiency virus, useful e.g. for therapy and diagnosis, have good solubility in water.
25	236	92.9	96	XX	XX

modulate interaction of Vpr with cellular factors, transcription-activating properties of Vpr, transport of Vpr and its incorporation into viral particles, Vpr-induced cell cycle arrest, and cytotoxic and ion-channel activities of Vpr. (1) is used to establish cell or animal models for studying pathogenicity of Vpr, for structural analysis of Vpr and its domains, for in vitro assembly of new vectors for gene therapy, in vitro or in vivo, for complementing the function of Vpr-defect mutants in cell cultures, and to reduce flexibility of Vpr induced by the N-terminal domain. Synthetic (1), are soluble in water and can be formulated as highly concentrated solutions (immolar) without protein aggregation, so are well suited to analysis by nuclear magnetic resonance, X-ray or circular dichroism techniques. (1) adopt a folded structure, have biological activity comparable to that of viral Vpr, and can be produced, at high purity, on the milligram scale. This sequence represents the synthetic HIV-1 derived Vpr peptide sVpr#48-96 which is used in the method of the invention

Sequence 49 AA;

Query Match 2

Score 100.0%; DB 3; Length 49;  
Best Local Similarity 100.0%; Pred. No. 7e-30;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDTRAGVEAIRILQQLPFHFRGCRHSRIGVTRQRRANGASRS 49

Db 1 ETYGDTRAGVEAIRILQQLPFHFRGCRHSRIGVTRQRRANGASRS 49

Synthetic.

PR

03-JUL-1992; 92US-00921104.

XX

PA (UYHA-) UNIV HAWAII.

XX

Hu W, Wang J;

XX

WPI; 1994-065685/08.

DR N-PSDB; AAQ48962.

New antisense viruses and anti-sense-ribozyme viruses - used for treating hepatitis B; HIV-2; SIV; flip-over PCR.

XX

PP 30-JUL-1993; 93WO-US007179.

XX

PR 30-JUL-1992; 92US-00921104.

XX

PA (UYHA-) UNIV HAWAII.

XX

Hu W, Wang J;

XX

WPI; 1994-065685/08.

DR N-PSDB; AAQ48962.

New antisense viruses and anti-sense-ribozyme viruses - used for treating hepatitis B; HIV-1, HIV-2 or SIV infection. Disclosure; Page 111; 167pp; English.

This sequence represents the "perfect" VPR protein encoded by the PCR fragment of pX-CS which encodes the truncated gag gene and the "perfect" vpr gene. The cDNA fragment encoding this protein was used to produce the antisense virus of the invention. Antisense or truncated RNAs expressed by these viruses bind to the mRNAs expressed by the naturally occurring viruses (NOVs) and prevent the NOVs from replicating. The antisense viruses thereby preventing the NOV from replicating. The antisense RNAs maintain the infectivity of the NOVs, allowing antisense RNAs to reach

the mRNAs of the natural viruses. Antisense viruses such as these may be used for treating or preventing a viral infection, particularly HIV-, HIV-2 or SIV infection or hepatitis B infection. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 49 AA;

Query Match 3

Score 100.0%; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 1.5e-29;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDTRAGVEAIRILQQLPFHFRGCRHSRIGVTRQRRANGASRS 49

Db 48 ETYGDTRAGVEAIRILQQLPFHFRGCRHSRIGVTRQRRANGASRS 96

RESULT 3

AAW53040 standard; peptide; 96 AA.

ID AAW53040

XX

AC AAW53040;

XX

DT 17-OCT-2003 (revised)

DT 17-JUL-1998 (first entry)

XX

DE HIV-1 polypeptide.

XX

Recombinant plant virus; HIV-1; protein production; immunisation; fusion capsid protein; alfalfa mosaic virus; ilarvirus; pathogen; rhabdovirus.

XX

KW Human immunodeficiency virus 1.

XX

OS Human immunodeficiency virus.

XX

PN WO9808375-A1.

XX

PD 05-MAR-1998.

XX

PP 28-AUG-1997;

XX

PR 28-AUG-1996;

XX

PA (UYJB-) UNIV JEFFERSON THOMAS.

XX

PI Koprowski H, Hooper DC, Yusibov V, Modelski A;

XX

DR WPI; 1998-179070/16.

XX

PT Production of poly-peptide(s), particularly for use in vaccines - by expression as fusion proteins with plant virus capsid protein in plant cells infected with virus.

XX

PS Disclosure; Page 4; 63pp; English.

XX

This sequence is a HIV-1 polypeptide that can be used in a recombinant plant virus used in the process of the invention. The process is for administering a polypeptide to an animal comprising: (a) infecting a plant cell with a recombinant plant virus nucleic acid that will be processed in a plant cell to produce a fusion capsid protein (FCP), and a polypeptide that is not a PVCP, the PVCP being an alfalfa mosaic virus (AlMV) capsid protein (CP) or ilarvirus CP thereby creating a infected cell; (b) cultivating the infected cell, or a derivative cell derived from the infected cell, under conditions where the infected cell or derivative cell makes the FCP; and (c) administering the FCP or a portion to an animal. The recombinant plant virus can also be used for production of polypeptides. The method is used particularly for the production of CC polypeptides which can be used for immunisation against pathogens such as CC rhabdovirus or HIV. (Updated on 17-OCT-2003 to standardise OS field)

SQ Sequence 96 AA;

Query Match 4

Score 254; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 1.5e-29;

Qy	1 ETYGDWAGVEAIIIRILQQLFIHRIGRHSRIGVTRQRARRNGASRS 49	Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	19-JAN-2001 (first entry)
Db	48 ETYGDWAGVEAIIIRILQQLFIHRIGRHSRIGVTRQRARRNGASRS 96		XX	HIV-1 regulatory virus protein R; Vpr; antiviral; gene therapy; pathogenicity; structural analysis; cell cycle arrest.
RESULT 4			XX	
AAB10049			OS Synthetic.	
ID AAB10049 standard; protein; 96 AA.			OS Human immunodeficiency virus 1.	
XX			XX	
AC AAB10049;			PN WO200049038-A2.	
XX			XX	
DT 12-SEP-2003 (revised)			PD 24-AUG-2000.	
DT 02-NOV-2000 (first entry)			XX	
DE HIV-1 vpr protein.			PF 19-FEB-2000; 2000WO-DE000525.	
XX			XX	
KW Glycoprotein; gag; pol; GP-1; GP-2; anti-HIV; cytostatic; gene therapy; treatment; infectious disease; HIV; AIDS; neoplasm; carcinoma; melanoma; vpr protein.			PR 19-FEB-1999; 99DB-01008752.	
XX			PR 19-FEB-1999; 99DB-01008766.	
OS Human immunodeficiency virus 1.			XX	
XX			PA (SCHU/ ) SCHUBERT U.	
PN EP1006196-A2.			PA (HENK/ ) HENKLEIN P.	
XX			PA (WRAY/ ) WRAY V.	
PD 07-JUN-2000.			XX	
XX			PI Schubert U, Henklein P, Wray V;	
PF 25-NOV-1999; 99EP-00250415.			XX	
XX			DR WPI; 2000-565367/52.	
PT 26-NOV-1998; 98DE-01056463.			XX	
XX			PT New synthetic peptides from the Vpr protein of human immunodeficiency virus, useful e.g. for therapy and diagnosis, have good solubility in water.	
PA (PETT-) PETTE INST HEINRICH.			XX	
XX			PS Claim 3.1; Page 5; 35DP; German.	
PI Von Laer MD;			XX	
XX			CC This invention describes novel synthetic peptides (I) derived from the HIV-1 regulatory viral protein R (Vpr) of human immunodeficiency virus-1 (HIV-1) which have antiviral activity and can be used for gene therapy. (I) is used for therapeutic and/or diagnostic purposes, especially in biological assays, for development of serological tests or enzyme-linked immunosorbent assays (ELISA) (e.g. for detecting or quantifying Vpr in blood), to raise specific antibodies and antiviral agents. (I) can also be used in screening for potential Vpr antagonists (i.e. compounds that modulate interaction of Vpr with cellular factors), transcription-activating properties of Vpr, transport of Vpr and its incorporation into viral particles. Vpr-induced cell cycle arrest, and cytotoxic and ion-channel activities of Vpr. (I) is used to establish cell or animal models for studying pathogenicity of Vpr, for structural analysis of Vpr and its domains, for in vitro assembly of new vectors for gene therapy, in vitro or in vivo, for complementing the function of Vpr-defect mutants in cell cultures, and to reduce flexibility of Vpr induced by the N-terminal domain. Synthetic (I), are soluble in water and can be formulated as highly concentrated solutions (amolar) without protein aggregation, so are well suited to analysis by nuclear magnetic resonance, X-ray or circular dichroism techniques. (I) adopt a folded structure, have biological activity comparable to that of viral Vpr, and can be produced, at high purity, on the milligram scale. This sequence represents the synthetic HIV-1 derived Vpr peptide svprl-96 which is used in the method of the invention	
DR 2000-378268/33.			XX	
DR N-PSDB; AAA40298, AAB10053, AAB10054.			CC	
XX			CC	
PT New retroviral packing cell useful as pharmaceutical carrier in gene therapy for treatment of HIV and neoplasms, comprises retroviral genes and glycoproteins.			CC	
PT			CC	
XX			CC	
PS Disclosure; Page 44; 69DP; German.			CC	
XX			CC	
PI Von Laer MD;			CC	
XX			CC	
DR 2000-378268/33.			CC	
DR N-PSDB; AAA40298, AAB10053, AAB10054.			CC	
XX			CC	
PT			CC	
XX			CC	
PS This invention describes a novel retroviral packing cell (I), comprising the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV coding gene gp, or a part of these. The products of the invention have anti-HIV and cytostatic activity and can be used for gene therapy. (I) is useful for in vitro infection of cells, especially hematopoietic stem cells, for expression of transgenes in cells and as a pharmaceutical carrier for gene therapy. (I) is therefore useful in the treatment of infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and other diseases. This sequence represents the Human immunodeficiency virus (HIV-1) vpr protein described in the method of the invention. (Updated on 12-SEP-2003 to standardise OS field)				
XX			CC	
PS Sequence 96 AA;			CC	
Query Match 100.0%; Score 254; DB 3; Length 96;			CC	
Best Local Similarity 100.0%; Pred. No. 1.5e-29;			CC	
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			CC	
Qy 1 ETYGDWAGVEAIIIRILQQLFIHRIGRHSRIGVTRQRARRNGASRS 49			CC	
Db 48 ETYGDWAGVEAIIIRILQQLFIHRIGRHSRIGVTRQRARRNGASRS 96			CC	
RESULT 5			CC	
ID AAB10685 standard; peptide; 96 AA.			CC	
XX			CC	
AC AAB10685;			CC	

RESULT 6  
AAB16129





SQ	Sequence 96 AA;	DT	22-APR-2004 (first entry)
	Query Match 100.0%; Score 254; DB 7; Length 96;	XX	
	Best Local Similarity 100.0%; Pred. No. 1.5e-29;	DE	HIV-1 Vpr protein.
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX		
QY	1 ERYGDTWAGVEAIRILQQLPHTFRIGCRHSRIGVTRQRARRGASRS 49	KW	HIV; Vpr; modulator; anti-HIV; virucide.
Db	48 ERYGDTWAGVEAIRILQQLPHTFRIGCRHSRIGVTRQRARRGASRS 96	XX	Human immunodeficiency virus type 1.
		OS	
		PN	W02003076621-A2.
		XX	
	RESULT 10	PD	18-SEP-2003.
ADF46812		XX	
ID ADF46812 standard; protein; 96 AA.	AC	PR	08-MAR-2002; 2002US-0362384P.
XX	XX	XX	
ACDF46812		PA	(UYMO-) UNIV MONTREAL.
DT 12-FEB-2004 (first entry)	XX	PI	Cohen EA, Yao X, Belhumeur P, Lemay J;
XX	XX	XX	
DE HIV-1 Vpr protein.	XX	DR	WPI; 2004-042337/04.
XX	XX	PT	New polypeptides that bind to viral Vpr protein, useful for treatment, prevention, diagnosis and prognosis of immune deficiency virus infection.
OS Human immunodeficiency virus 1.	XX	PT	
JP2003259881-A.	XX	PS	Example 20; Page 33-34; 143pp; English.
PN	XX	XX	
XX	XX	CC	The present invention relates to peptide which are capable of binding to the HIV protein Vpr and/or modulates Vpr-related activity. Such peptides are used for prevention, treatment, diagnosis and prognosis of Vpr-related diseases, particularly lentiviral infection (specifically HIV-1 or -2, or simian immune deficiency virus), for modulating, particularly inhibiting, Vpr-related activities and for detecting Vpr in a sample.
XX	XX	CC	Nucleic acids encoding such peptides and cells that contain this nucleic acid can also be used therapeutically. The present sequence is a protein of relevance to the invention.
XX	XX	CC	
XX	XX	CC	Sequence 96 AA;
XX	XX	Query Match 100.0%; Score 254; DB 8; Length 96;	
XX	XX	Best Local Similarity 100.0%; Pred. No. 1.5e-29;	
XX	XX	Mismatches 0; Indels 0; Gaps 0;	
PS Claim 1; SEQ ID NO 1; 14pp; Japanese.	Qy	1	ETYGDTWAGVEAIRILQQLPHTFRIGCRHSRIGVTRQRARRGASRS 49
XX	Db	48	ETYGDTWAGVEAIRILQQLPHTFRIGCRHSRIGVTRQRARRGASRS 96
XX	XX	RESULT 12	
XX	XX	ADP20070	
XX	XX	ID ADP20070 standard; protein; 96 AA.	
XX	XX	ADP20070;	
XX	XX	AC	
XX	XX	DT 09-SEP-2004 (first entry)	
XX	XX	XX	
XX	XX	DE Human immunodeficiency virus 1 isolate JRCSF vpr protein.	
XX	XX	XX	
XX	XX	XX	immunogenic mutant HIV gp120; human immunodeficiency virus; HIV; gp120; immunogenic; vaccine; HIV neutralising antibody; anti-HIV; HIV binding agent; immunisation; HIV-1; infection; HIV-1 isolate JRCSF;
XX	XX	XX	
XX	XX	OS Human immunodeficiency virus 1.	
XX	XX	PN W02004053100-A2.	
XX	XX	PD 24-JUN-2004.	
XX	XX	PF 11-DEC-2003; 2003WO-WO033534.	
XX	XX	PR 11-DEC-2002; 2002US-0432869P.	
XX	XX	PR 24-APR-2003; 2003US-0465350P.	
RESULT 11			
ABM79669			
ID ABM79669 standard; protein; 96 AA.	XX		
XX	AC ABM79669.		
XX	XX		



XX WPI; 1996-171615/17.  
 DR Targetting mature HIV virion(s) using HIV Vpr, Vpx or p6 proteins - for  
 PT affecting structural organisation or function or for inhibiting  
 PT replication.  
 XX  
 PS Claim 8; Page 43; 68pp; English.  
 XX The present sequence is the native Vpr protein from the HIV-1 LAI strain  
 CC isolate, which can be used in the development of a chimaeric mol.  
 CC comprising the present sequence and another mol., pref. a HIV infectivity  
 CC or replication reducing protein fragment, i.e., a RNase and/or protease, a  
 CC virion assembly and/or morphogenesis steric hindrance inducer and/or an  
 CC effector of a viral protein interaction responsible for viral infectivity  
 CC and/or replication. The chimaeric mol. can be specifically targetted into  
 CC the mature HIV-1 virion, to affect its structural organisation and/or  
 CC functional integrity, i.e. gene therapy of HIV-1 infection. Vpr protein  
 CC fragments can also be used to prevent viral replication by interfering  
 CC with the protein interactions responsible for Vpr incorporation into the  
 CC mature HIV-1 genome. (Updated on 16-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 96 AA;

Query Match 98.4%; Score 250; DB 2;  
 Best Local Similarity 98.0%; Pred. No. 5.8e-29; Length 96;  
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ETYGDWTAGVEAIIIRLQLLFIHRIGCRHSRIGVTQQRARGASRS 49  
 Db 48 ETYGDWTAGVEAIIIRLQLLFIHRIGCRHSRIGVTQQRARGASRS 96

## RESULT 15

AA53247  
 ID AAY53247 standard; protein; 96 AA.  
 XX  
 AC AAY53247;  
 XX DT 12-SEP-2003 (revised)  
 DT 17-JUL-2000 (first entry)  
 XX DE HIV-1 LAI strain Vpr protein SEQ ID NO:1.  
 XX HIV-1; HIV-2; virion; Vpr; Vpx; p6; chimeric; infection; anti-HIV;  
 KW gene therapy.  
 XX OS Human immunodeficiency virus 1.  
 XX PN US6043081-A.  
 XX PD 28-MAR-2000.  
 XX PF 07-SEP-1995; 95US-00524694.  
 XX PR 07-SEP-1994; 94US-00301915.  
 PA (TUMO-) UNIV MONTREAL.

XX Yao X, Pignac-Kobinger G, Checroune F, Cohen EA, Bergeron D;  
 XX DR WPI; 2000-270343/23.  
 PT Expression vector useful for reducing infectivity of HIV or for targeting  
 PT into HIV virions, comprises nucleic acid segment encoding recombinant or  
 XX chimeric protein comprising a Vpr/vpx virion incorporation domain.  
 PS Claim 1; Col 7-8; 32pp; English.  
 XX  
 CC The present invention describes an expression vector (I) comprising a  
 CC nucleic acid segment encoding a recombinant protein for interfering with  
 CC the incorporation of native Vpr/vpx into HIV-1 or HIV-2 virion or a  
 CC chimeric protein that is incorporated into an HIV-1 or HIV-2 virion,

CC operably linked to a promoter. Also described are: (1) an isolated  
 CC eukaryotic or prokaryotic cell transfectable with (I); (2) a composition  
 CC for reducing infectivity of HIV-1 or HIV-2 in vitro comprising an  
 CC effective amount of (I) in association with a pharmaceutically acceptable  
 CC carrier; and (3) a composition for targeting into an HIV-1 or HIV-2  
 CC virion comprising an effective amount of (I) in association with a  
 CC pharmaceutically acceptable carrier. (I) has anti-HIV activity and can be  
 CC used in gene therapy. (I) is useful for reducing infectivity of HIV in  
 CC vitro and for targeting into an HIV-1 or HIV-2 virion. The present  
 CC sequence represents the Vpr protein from an HIV-1 strain, which is used  
 CC in the exemplification of the present invention. (Updated on 12-SEP-2003  
 CC to standardise OS field)  
 XX  
 SQ Sequence 96 AA;

Query Match 98.4%; Score 250; DB 3;  
 Best Local Similarity 98.0%; Pred. No. 5.8e-29;  
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ETYGDWTAGVEAIIIRLQLLFIHRIGCRHSRIGVTQQRARGASRS 49  
 Db 48 ETYGDWTAGVEAIIIRLQLLFIHRIGCRHSRIGVTQQRARGASRS 96

Search completed: October 18, 2004, 18:45:33  
 Job time : 65.3125 secs

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2004, 18:42:45 ; Search time 28.5833 Seconds (without alignments)

113.688 Million cell updates/sec

Title: US-09-913-927D-3

Perfect score: 254

Sequence: 1 ETYGDTWAGVBEAIRLQLQL.....RHSRIGVTRRARGASRS 49

Scoring table: BIOSUM62

Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:  
1: /cn2\_6/podata/1/iaa/5A COMB.pep:  
2: /cn2\_6/podata/1/iaa/5B COMB.pep:  
3: /cn2\_6/podata/1/iaa/6A COMB.pep:  
4: /cn2\_6/podata/1/iaa/6B COMB.pep:  
5: /cn2\_6/podata/1/iaa/9CTVS COMB.pep:  
6: /cn2\_6/podata/1/iaa/backfiles.pep:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution. and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	254	100.0	96	4	US-09-309-572-19
2	254	100.0	96	4	US-09-718-096-19
3	254	100.0	96	4	US-09-839-329-1
4	250	98.4	96	2	US-08-301-915-1
5	250	98.4	96	3	US-08-524-694A-1
6	250	98.4	96	4	US-09-454-156A-1
7	249	98.0	96	3	US-08-704-856C-15
8	249	82.9	95	4	US-09-242-881-15
9	210.5	77.6	100	4	US-09-462-917A-118
10	197	75.6	100	4	US-09-462-917A-115
11	192	70.5	100	4	US-09-462-917A-116
12	179	67.7	93	4	US-09-462-917A-117
13	172	52.0	78	3	US-09-124-900-5
14	132	51.6	72	3	US-08-301-915-4
15	131	51.6	72	3	US-08-524-694A-4
16	131	51.6	72	4	US-09-454-156A-4
17	131	45.7	105	4	US-03-454-156A-2
18	123	48.4	24	4	US-09-839-329-2
19	119.5	47.0	3077	6	5223423
20	117	46.1	100	4	US-03-206-551-49
21	116	45.7	105	2	US-08-301-915-2
22	116	45.7	105	3	US-08-524-694A-2
23	116	45.7	105	4	US-03-454-156A-2
24	105	41.3	105	2	US-08-659-251-9
25	105	41.3	105	3	US-09-256-490-9
26	105	41.3	105	5	PCT-US96-1445-9
27	94	37.0	18	4	US-09-839-329-3

ALIGNMENTS

RESULT 1

US-09-309-572-19

; Sequence 19, Application US/09309572

; Patent No. 6440730

; GENERAL INFORMATION:

; APPLICANT: Heinrich-Pette-Institut

; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV

; FILE REFERENCE: P50489

; CURRENT APPLICATION NUMBER: US/09/309,572

; CURRENT FILING DATE: 1999-05-11

; EARLIER APPLICATION NUMBER: DE 198 56 463

; EARLIER FILING DATE: 1998-11-26

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

; FEATURE:

; OTHER INFORMATION: vpr protein

US-09-309-572-19

Query Match 100.0% ; Score 254; DB 4; Length 96;

Best Local Similarity 100.0%; Pred. No. 78-31;

Matches 49; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 ETYGDTWAGVBEAIRLQLQLFHPRICRHSRIGVTRQRARRANGASRS 49

Db 48 ETYGDTWAGVBEAIRLQLQLFHPRICRHSRIGVTRQRARRANGASRS 96

RESULT 2

US-09-718-096-19

; Sequence 19, Application US/09718096

; Patent No. 6583763

; GENERAL INFORMATION:

; APPLICANT: Von Laer, Meike-Dorothee

; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV

; FILE REFERENCE: 35-195

; CURRENT APPLICATION NUMBER: US/09/718,096

; CURRENT FILING DATE: 2000-11-22

; PRIOR APPLICATION NUMBER: DE 19856463,5

; PRIOR FILING DATE: 1998-11-16

; PRIOR APPLICATION NUMBER: EP 99250415,9

; PRIOR FILING DATE: 1999-11-25

; PRIOR APPLICATION NUMBER: US 09/309,572

; PRIOR FILING DATE: 1999-05-11

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

LENGTH: 96  
 TYPE: PRT  
 ORGANISM: Human immunodeficiency virus type 1  
 FEATURE:  
 OTHER INFORMATION: vpr protein  
 US-09-718-096-19

Query Match 100.0%; Score 254; DB 4; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 7e-31; Indels 0; Gaps 0;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIIIRLQQLLTHFRGCRHSRIGTVTQRRAANGAARS 49  
 Db 48 ETYGDWTAGVEAIIIRLQQLLTHFRGCRHSRIGTVTQRRAANGAARS 96

RESULT 3  
 US-09-839-329-1  
 Sequence 1, Application US/09839329

GENERAL INFORMATION:  
 APPLICANT: Michael P. Sherman  
 APPLICANT: Warner C. Greene  
 APPLICANT: Carlos M.C. de No. 6664040china  
 APPLICANT: Ulrich Schubert  
 APPLICANT: Peter Henklein  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF  
 FILE REFERENCE: G&C 30448.91-002  
 CURRENT APPLICATION NUMBER: US/09-839,329  
 CURRENT FILING DATE: 2001-04-20  
 PRIOR APPLICATION NUMBER: 60/206,610  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR FILING DATE: 2001-02-09  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 96

ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic peptide of regulatory virus proteins R  
 OTHER INFORMATION: (ypr) of human immunodeficiency virus type 1  
 OTHER INFORMATION: (HIV-1)

US-09-839-329-1

Query Match 100.0%; Score 254; DB 4; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 7e-31; Indels 0; Gaps 0;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIIIRLQQLLTHFRGCRHSRIGTVTQRRAANGAARS 49  
 Db 48 ETYGDWTAGVEAIIIRLQQLLTHFRGCRHSRIGTVTQRRAANGAARS 96

RESULT 4  
 US-08-301-915-1  
 Sequence 1, Application US/08301915  
 Patent No. 5,861,161  
 GENERAL INFORMATION:  
 APPLICANT: COHEN, Eric A.  
 APPLICANT: BERGERON, Dominique  
 APPLICANT: CHERECOURNE, Florent  
 APPLICANT: YAO, Xiao-Jian  
 APPLICANT: PIGNAC-KOBINGER, Gary  
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS  
 TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KLAUBER & JACKSON  
 STREET: Continental Plaza, 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: N.J.  
 COUNTRY: U.S.A.

ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/301,915  
 FILING DATE: September 7, 1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JACKSON, David A.  
 REGISTRATION NUMBER: 201-487-5800  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-343-1684  
 TELEFAX: 201-343-1684

RESULT 5  
 US-08-524-694A-1  
 Sequence 1, Application US/08524694A  
 Patent No. 6043081  
 GENERAL INFORMATION:  
 APPLICANT: COHEN, Eric A.  
 APPLICANT: BERGERON, Dominique  
 APPLICANT: CHERECOURNE, Florent  
 APPLICANT: YAO, Xiao-Jian  
 APPLICANT: PIGNAC-KOBINGER, Gary  
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS BASED  
 TITLE OF INVENTION: ON HIV-1 VPR FUSION MOLECULES  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KLAUBER & JACKSON  
 STREET: Continental Plaza, 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: N.J.  
 COUNTRY: U.S.A.

ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/524,694A  
 FILING DATE: September 7, 1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JACKSON, David A.  
 REGISTRATION NUMBER: 201-487-5800  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-343-1684  
 TELEFAX: 201-343-1684

TELEX: 133521  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO

US-08-524-694A-1

RESULT 6

Query Match 98.4%; Score 250; DB 3; Length 96;  
 Best Local Similarity 98.0%; Pred. No. 2.8e-30;  
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQQLFIRIGCRHSRIGVTRQRARGASRS 49  
 Db 48 ETYGDWTAGVEAIRILQQLFIRIGCRHSRIGVTRQRARGASRS 96

US-09-454-156A-1

Sequence 1, Application US/09454156A  
 Patent No. 6468539

GENERAL INFORMATION:  
 APPLICANT: COHEN, Eric A.  
 APPLICANT: BERGERON, Dominique  
 APPLICANT: CHECROUET, Florent  
 APPLICANT: YAO, Xiao-Jian  
 APPLICANT: PIGNAC-KOBINGER, Gary  
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS  
 TITLE OF INVENTION: BASED ON HIV-1 VPR FUSION MOLECULES  
 NUMBER OF SEQUENCES: 5  
 COUNTRY: U.S.A.  
 ZIP: 07601

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/454,156A  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/301,915  
 FILING DATE:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO

US-09-454-156A-1

Query Match 98.4%; Score 250; DB 4; Length 96;  
 Best Local Similarity 98.0%; Pred. No. 2.8e-30;  
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQQLFIRIGCRHSRIGVTRQRARGASRS 49  
 Db 48 ETYGDWTAGVEAIRILQQLFIRIGCRHSRIGVTRQRARGASRS 96

RESULT 7

Query Match 98.0%; Score 249; DB 3; Length 96;  
 Best Local Similarity 98.0%; Pred. No. 4e-30; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQQLFIRIGCRHSRIGVTRQRARGASRS 49  
 Db 48 ETYGDWTAGVEAIRILQQLFIRIGCRHSRIGVTRQRARGASRS 96

US-08-704-856C-15

Sequence 15, Application US/08704856C  
 Patent No. 6442832

GENERAL INFORMATION:  
 APPLICANT: Koprowski, Hilary  
 APPLICANT: Yusibov, Vladi  
 APPLICANT: Hooper, Douglas, C.  
 APPLICANT: Modelski, Anna  
 TITLE OF INVENTION: Polypeptides Fused with Plant Virus  
 TITLE OF INVENTION: Coat Proteins  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Allan H. Fried & Associates  
 STREET: 1525 Locust Street, 15th Floor  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: USA  
 ZIP: 19102

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Corel WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/704,856C  
 FILING DATE: 28-Aug-1996  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fried, Allan H.  
 REGISTRATION NUMBER: 31,253  
 REFERENCE DOCKET NUMBER: T19-007  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 732-7090  
 TELEFAX: (215) 732-7090  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 HYPOTHETICAL: N

US-08-704-856C-15

Query Match 98.0%; Score 249; DB 3; Length 96;  
 Best Local Similarity 98.0%; Pred. No. 4e-30; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQQLFIRIGCRHSRIGVTRQRARGASRS 49  
 Db 48 ETYGDWTAGVEAIRILQQLFIRIGCRHSRIGVTRQRARGASRS 96

RESULT 8

Query Match 98.0%; Score 249; DB 3; Length 96;  
 Best Local Similarity 98.0%; Pred. No. 4e-30; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQQLFIRIGCRHSRIGVTRQRARGASRS 49  
 Db 48 ETYGDWTAGVEAIRILQQLFIRIGCRHSRIGVTRQRARGASRS 96

US-09-242-881-15

Sequence 15, Application US/09242881  
 Patent No. 6440700

GENERAL INFORMATION:  
 APPLICANT: Koprowski, Hilary  
 APPLICANT: Yusibov, Vladi  
 APPLICANT: Hooper, Douglas, C.  
 APPLICANT: Modelski, Anna  
 TITLE OF INVENTION: Polypeptides Fused with Plant Virus  
 TITLE OF INVENTION: Coat Proteins  
 NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Allan H. Fried & Associates  
 STREET: 1525 Locust Street, 15th Floor  
 CITY: Philadelphia

STATE: Pennsylvania  
 COUNTRY: USA  
 ZIP: 19102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy Disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Corel WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/242,881  
 FILING DATE: 25-Mar-1999  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/704,856  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fried, Allan H.  
 REGISTRATION NUMBER: 31,253  
 REFERENCE/DOCKET NUMBER: T19-007  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 732-7090  
 TELEFAX: (215) 732-7090  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 96 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 HYPOTHETICAL: N  
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 US-09-242-881-15

Query Match  
 Best Local Similarity 98.0%; Score 249; DB 4; Length 96;  
 Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 ETYGDTWAGVEAIRLQLQQLFHRIGCRHSRIGVTRQRARGASRS 49  
 Db 48 ETYGDTWAGVEAIRLQLQQLFHRIGCRHSRIGVTRQRARGASRS 96

RESULT 9  
 US-09-319-58BC-10  
 / Sequence 10, Application US/0931958BC  
 / Patent No. 6509018  
 / GENERAL INFORMATION:  
 / APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE-INERM  
 / APPLICANT: ASSISTANCE PUBLIQUE-HOPITAUX DE PARIS  
 / APPLICANT: INSTITUT PASTEUR  
 / APPLICANT: MAUCLERE, Philippe  
 / APPLICANT: LOUSSER-AJAKA, Ibtissam  
 / APPLICANT: SIMON, Francois  
 / APPLICANT: SARAGOSTI, Sento  
 / APPLICANT: BARRE-SINOUSSI, Francoise  
 / TITLE OF INVENTION: NON-M NON-O HIV STRAINS, FRAGMENTS AND APPLICATIONS.  
 / CURRENT APPLICATION NUMBER: US/09/319,588C  
 / CURRENT FILING DATE: 1999-08-27  
 / PRIOR APPLICATION NUMBER: FR96/15087  
 / PRIOR FILING DATE: 1996-12-09  
 / NUMBER OF SEQ ID NOS: 98  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO 10  
 / LENGTH: 95  
 / TYPE: PRT  
 / ORGANISM: Human immunodeficiency virus type 1  
 / US-09-319-588C-10

Query Match  
 Best Local Similarity 82.9%; Score 210; DB 4; Length 95;  
 Matches 41; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Db 2 TYGDTWAGVEAIRLQLQQLFHRIGCRHSRIGVTRQRARGASRS 49  
 Db 48 ETYGDTWAGVEAIRLQLQQLFHRIGCRHSRIGVTRQRARGASRS 100

RESULT 10  
 US-09-462-917A-118  
 / Sequence 118, Application US/09462917A  
 / Patent No. 6511801  
 / GENERAL INFORMATION:  
 / APPLICANT: Delaporte, Eric  
 / APPLICANT: Peeters, Martine  
 / APPLICANT: Saman, Eric  
 / APPLICANT: Vanden Haesevelde, Marlen  
 / TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof  
 / FILE REFERENCE: INNS:014 11162.0014.NPUS00  
 / CURRENT APPLICATION NUMBER: US/09/462,917A  
 / CURRENT FILING DATE: 2000-04-03  
 / PRIOR APPLICATION NUMBER: PCT/EP98/04522  
 / PRIOR FILING DATE: 1998-07-20  
 / NUMBER OF SEQ ID NOS: 152  
 / SOFTWARE: PatentIn version 3.0  
 / SEQ ID NO 118  
 / LENGTH: 100  
 / TYPE: PRT  
 / ORGANISM: Human  
 / US-09-462-917A-118

Query Match  
 Best Local Similarity 77.6%; Score 197; DB 4; Length 100;  
 Matches 39; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

Qy 1 ETYGDTWAGVEAIRLQLQQLFHRIGCRHSRIGVTRQRARGASRS 49  
 Db 48 ETYGDTWAGVEAIRLQLQQLFHRIGCRHSRIGVTRQRARGASRS 100

RESULT 11  
 US-09-462-917A-115  
 / Sequence 115, Application US/09462917A  
 / Patent No. 6511801  
 / GENERAL INFORMATION:  
 / APPLICANT: Delaporte, Eric  
 / APPLICANT: Peeters, Martine  
 / APPLICANT: Saman, Eric  
 / APPLICANT: Vanden Haesevelde, Marlen  
 / TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof  
 / FILE REFERENCE: INNS:014 11162.0014.NPUS00  
 / CURRENT APPLICATION NUMBER: US/09/462,917A  
 / CURRENT FILING DATE: 2000-04-03  
 / PRIOR APPLICATION NUMBER: PCT/EP98/04522  
 / PRIOR FILING DATE: 1998-07-20  
 / NUMBER OF SEQ ID NOS: 152  
 / SOFTWARE: PatentIn version 3.0  
 / SEQ ID NO 115  
 / LENGTH: 100  
 / TYPE: PRT  
 / ORGANISM: Human  
 / US-09-462-917A-115

Query Match  
 Best Local Similarity 73.6%; Score 197; DB 4; Length 100;  
 Matches 39; Conservative 4; Mismatches 6; Indels 4; Gaps 1;

Qy 1 ETYGDTWAGVEAIRLQLQQLFHRIGCRHSRIGVTRQRARGASRS 49  
 Db 48 ETYGDTWAGVEAIRLQLQQLFHRIGCRHSRIGVTRQRARGASRS 100

RESULT 12  
 US-09-462-917A-116  
 / Sequence 116, Application US/09462917A  
 / Patent No. 6511801  
 / GENERAL INFORMATION:  
 / APPLICANT: Delaporte, Eric

APPLICANT: Peeters, Martine  
 APPLICANT: Saman, Eric  
 APPLICANT: Vanden Heeselde, Marlen  
 TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof  
 FILE REFERENCE: INNS:014 11362.0014.NPUS00  
 CURRENT APPLICATION NUMBER: US/09/462,917A  
 CURRENT FILING DATE: 2000-04-03  
 PRIOR APPLICATION NUMBER: PCT/EP98/04522  
 PRIOR FILING DATE: 1998-07-20  
 NUMBER OF SEQ ID NOS: 152  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 116  
 LENGTH: 100  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-462-917A-116

Query Match 70.5%; Score 179; DB 4; Length 100;  
 Best Local Similarity 65.4%; Pred. No. 1.7e-19;  
 Matches 34; Conservative 7; N mismatches 7; Indels 4; Gaps 1;

Qy 1 ETYGDWTAGVETAIRLQLQFLFRRGHSRIGV---TQRQRARNASR 48  
 Db 48 ETYGDWTAGVETAIRLQLQFLFRRGHSRIGV---TQRQRARNASR 48

RESULT 13  
 US-09-462-917A-117  
 Sequence 117, Application US/09462917A  
 Patent No. 6511801  
 GENERAL INFORMATION:  
 APPLICANT: Delaporte, Eric  
 APPLICANT: Peeters, Martine  
 APPLICANT: Saman, Eric  
 APPLICANT: Vanden Heeselde, Marlen  
 TITLE OF INVENTION: HIV-1 Group O Antigens and Uses Thereof  
 FILE REFERENCE: INNS:014 11362.0014.NPUS00  
 CURRENT APPLICATION NUMBER: US/09/462,917A  
 CURRENT FILING DATE: 2000-04-03  
 PRIOR APPLICATION NUMBER: PCT/EP98/04522  
 PRIOR FILING DATE: 1998-07-20  
 NUMBER OF SEQ ID NOS: 152  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 117  
 LENGTH: 93  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-462-917A-117

Query Match 67.7%; Score 172; DB 4; Length 93;  
 Best Local Similarity 63.8%; Pred. No. 1.8e-18;  
 Matches 31; Conservative 3; N mismatches 3; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVETAIRLQLQFLFRRGHSRIGV 37  
 Db 48 ETYGDWTAGVETAIRLQLQFLFRRGHSRIGV 34

RESULT 14  
 US-09-124-900-5  
 Sequence 5, Application US/09124900  
 Patent No. 6268484  
 GENERAL INFORMATION:  
 APPLICANT: KATINGER, Hermann  
 APPLICANT: BUCHACHER, Andrea  
 APPLICANT: ERNST, Wolfgang  
 APPLICANT: BALLAUN, Claudia  
 APPLICANT: PERTSCHER, Martin  
 APPLICANT: TIKOLA, Alexandra  
 APPLICANT: PREDL, Renate  
 APPLICANT: SCHMIDT, Christine  
 APPLICANT: KLIMA, Annelies  
 APPLICANT: STINDL, Franz

Query Match 51.6%; Score 131; DB 2; Length 72;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-12;  
 Matches 25; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

APPLICANT: MUSTER, Thomas  
 TITLE OF INVENTION: HIV-Vaccines  
 FILE REFERENCE: 1939-112.P  
 CURRENT APPLICATION NUMBER: US/09/1124,900  
 CURRENT FILING DATE: 1998-07-30  
 PRIOR APPLICATION NUMBER: PCT/EP95/01481  
 PRIOR FILING DATE: 1995-04-19  
 NUMBER OF SEQ ID NOS: 11  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 5  
 LENGTH: 78  
 TYPE: PRT  
 ORGANISM: Human immunodeficiency virus type 1  
 US-09-124-900-5

Query Match 52.0%; Score 132; DB 3; Length 78;  
 Best Local Similarity 96.2%; Pred. No. 1.7e-12;  
 Matches 25; Conservative 1; N mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVETAIRLQLQFLFRR 26  
 Db 48 ETYGDWTAGVETAIRLQLQFLFRR 73

RESULT 15  
 US-08-301-915-4  
 Sequence 4, Application US/08301915  
 Patent No. 5861161  
 GENERAL INFORMATION:  
 APPLICANT: COHEN, Eric A.  
 APPLICANT: BERGERON, Dominique  
 APPLICANT: CHECROUNE, Florent  
 APPLICANT: YAO, Xiao-Jian  
 APPLICANT: PIGNAC-KOBINGER, Gary  
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV VIRIONS  
 TITLE OF INVENTION: PROTEIN TARGETING INTO HIV-1 VPR FUSION MOLECULES  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: KLAUBER & JACKSON  
 STREET: Continental Plaza, 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: N.J.  
 COUNTRY: U.S.A.  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/301,915  
 FILING DATE:  
 CLASSIFICATION: 536  
 TELEFAX: 201-487-5800  
 TELLEX: 133521  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 72 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 US-08-301-915-4

Query Match 51.6%; Score 131; DB 2; Length 72;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-12;  
 Matches 25; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIIIRIIQQLLFIHF 25  
Db 48 ETYGDWTAGVEAIIIRIIQQLLFIHF 72

Search completed: October 18, 2004, 18:49:23  
Job time : 29.5833 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	254	100.0	96	9 US-09-839-329-1	Sequence 1, Appl1
2	254	100.0	96	14 US-10-055-261-272	Sequence 272, App
3	254	100.0	96	14 US-10-190-435-284	Sequence 284, App
4	240	94.5	96	14 US-10-190-435-272	Sequence 272, App
5	239	94.1	96	14 US-10-190-435-285	Sequence 285, App
6	238	93.7	96	14 US-10-190-435-262	Sequence 262, App
7	235	92.5	96	14 US-10-190-435-274	Sequence 274, App
8	235	92.5	96	14 US-10-190-435-278	Sequence 278, App
9	234	92.1	96	14 US-10-190-435-263	Sequence 263, App
10	234	92.1	96	14 US-10-190-435-273	Sequence 273, App
11	234	92.1	96	14 US-10-190-435-276	Sequence 276, App
12	233	91.7	96	14 US-10-190-435-264	Sequence 264, App
13	233	91.7	96	14 US-10-190-435-265	Sequence 265, App
14	233	91.7	96	14 US-10-190-435-266	Sequence 266, App

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2004, 18:43:30 ; Search time 88.8125 Seconds  
(without alignments)

178.383 Million cell updates/sec

Title: US-09-913-927D-3

Perfect score: 254

Sequence: 1 ETYGDTWAGVEAIIRLQQL.....RHSRIGVTRORRANGASRS 49

Scoring table: BILOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6\_ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6\_ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

3: /cgn2\_6\_ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

4: /cgn2\_6\_ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6\_ptodata/2/pubpaa/PCRS\_PUBCOMB.pep:\*

6: /cgn2\_6\_ptodata/2/pubpaa/PCTRS\_PUBCOMB.pep:\*

7: /cgn2\_6\_ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

8: /cgn2\_6\_ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

9: /cgn2\_6\_ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6\_ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6\_ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6\_ptodata/2/pubpaa/US09\_New\_PUBCOMB.pep:\*

13: /cgn2\_6\_ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6\_ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6\_ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6\_ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*

17: /cgn2\_6\_ptodata/2/pubpaa/US10\_E\_PUBCOMB.pep:\*

18: /cgn2\_6\_ptodata/2/pubpaa/US60\_New\_PUBCOMB.pep:\*

19: /cgn2\_6\_ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

RESULT 1 ; Publication US-09839329-1

; General Information: US20020022027A1

; Applicant: Michael P. Sherman

; Inventor: Warner C. Greene

; Applicant: Carlos M.C. de No. 6664040ohna

; Applicant: Ulrich Schubert

; Applicant: Peter Henlein

; Title of Invention: Compositions and Methods for Delivery of a Molecule into a Cell

; Title of Invention: Compositions and Methods for Delivery of

; Title of Invention: (YDPR) of Human Immunodeficiency Virus Type 1

; File Reference: GEC 30448-91-US-U2

; Current Application Number: US-09-839-329

; Current Filing Date: 2001-04-20

; Prior Application Number: 60/206,610

; Prior Filing Date: 2000-05-23

; Prior Application Number: 60/267,827

; Prior Filing Date: 2001-02-09

; Number of SEQ ID NOS: 5

; Software: FastEQ for Windows Version 4.0

Qy 1 ETYGDTWAGVEAIIRLQQLFHRIGRHSIGVTRORRANGASRS 49

Db 48 ETYGDTWAGVEAIRILQQLLFIHRIGCRHSRIGVTRQRARRGASRS 96

; Sequence 272, Application US/10190435

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

;

RESULT 2

US-10-059-261-272

; Sequence 272, Application US/10059261

; Publication No. US20030077826A1

; GENERAL INFORMATION:

; APPLICANT: EDELMAN, LENA

; JACOTOT, ETIENNE DANIEL FRANCOIS

; BRIAND, JEAN-PAUL

; CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET

; SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC

; FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX

; (PTPC)

; FILE REFERENCE: 03435.0216

; CURRENT APPLICATION NUMBER: US/10/059,261

; CURRENT FILING DATE: 2002-08-29

; PRIORITY NUMBER: 60/0265,594

; PRIORITY FILING DATE: 2001-02-02

; NUMBER OF SEQ ID NOS: 325

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 272

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

; US-10-059-261-272

; Query Match Score 100.0%;

; Best Local Similarity 100.0%;

; Pred. No. 1.5e-28;

; Length 96;

; Indels 0;

; Gaps 0;

; OTHER INFORMATION: Description of Artificial Sequence: Vpr HXB2

; SEQ ID NO 284

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 285

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 286

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 287

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 288

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 289

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 290

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 291

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 292

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 293

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 294

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

RESULT 3

US-10-190-435-284

; Sequence 284, Application US/10190435

; Publication No. US2003013248A1

; GENERAL INFORMATION:

; APPLICANT: ZUR MEGEDE, JAN

; LIAN, YING

; ENGELBRECHT, SUSAN

; VAN RENSBURG, ESTRELITA J.

; CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET

; SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC

; FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX

; (PTPC)

; FILE REFERENCE: PP18133.003 / 2302-18133

; CURRENT APPLICATION NUMBER: US/10/190,435

; CURRENT FILING DATE: 2002-12-30

; NUMBER OF SEQ ID NOS: 319

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 284

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 285

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 286

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 287

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 288

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 289

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 290

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 291

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 292

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 293

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 294

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 295

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 296

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 297

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

RESULT 4

US-10-190-435-284

; Sequence 284, Application US/10190435

; Publication No. US2003013248A1

; GENERAL INFORMATION:

; APPLICANT: ZUR MEGEDE, JAN

; LIAN, YING

; ENGELBRECHT, SUSAN

; VAN RENSBURG, ESTRELITA J.

; CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET

; SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOTIC

; FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX

; (PTPC)

; FILE REFERENCE: PP18133.003 / 2302-18133

; CURRENT APPLICATION NUMBER: US/10/190,435

; CURRENT FILING DATE: 2002-12-30

; NUMBER OF SEQ ID NOS: 319

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 284

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 285

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 286

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 287

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 288

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 289

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: Vpr Consensus

; SEQ ID NO 290

; LENGTH: 96

; TYPE: PRT

```

; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 278
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vpr 301905-ind
; US-10-190-435-278

Query Match 92.5%; Score 235; DB 14; Length 96;
Best Local Similarity 87.8%; Pred. No. 8.2e-26;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTGVEAIRLQLLFIHRIGRHSRIGVTRQRARRGASRS 49
Db 48 ETYGDWTGVEAIRLQLLFIHRIGRHSRIGVTRQRARRGASRS 96

RESULT 9
US-10-190-435-263
; Sequence 263, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Eberlita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 263
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vpr TV001-2
; US-10-190-435-263

Query Match 92.1%; Score 234; DB 14; Length 96;
Best Local Similarity 87.8%; Pred. No. 1.1e-25;
Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTGVEAIRLQLLFIHRIGRHSRIGVTRQRARRGASRS 49
Db 48 ETYGDWTGVEAIRLQLLFIHRIGRHSRIGVTRQRARRGASRS 96

RESULT 10
US-10-190-435-273
; Sequence 273, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Eberlita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0

RESULT 8
US-10-190-435-278
; Sequence 278, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Eberlita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0

```



Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 ETYGDWTAGVBAIRILQLFIHRIGCRHSRIGVTRQRARRGASRS 49  
 Db 48 DTYGDWTAGVBAIRILQLFIHRIGCRHSRIGVTRQRARRGASRS 96

---

RESULT 15  
 US-10-190-435-270  
 Sequence 270, Application US/10190435  
 Publication No. US20030143248A1  
 GENERAL INFORMATION:  
 APPLICANT: ZUR MEGEDE, Jan  
 APPLICANT: BARNETT, Susan W.  
 APPLICANT: LIAN, Ying  
 APPLICANT: ENGELBRECHT, Susan  
 APPLICANT: VAN RENSBURG, Estrelita J.  
 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  
 TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  
 FILE REFERENCE: PP18133.003 / 2302-18133  
 CURRENT APPLICATION NUMBER: US/10/190,435  
 CURRENT FILING DATE: 2002-12-30  
 NUMBER OF SEQ ID NOS: 319  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 270  
 LENGTH: 96  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Vpr TV003-12

US-10-190-435-270  
 Query Match 91.7%; Score 233; DB 14; Length 96;  
 Best Local Similarity 87.8%; Pred. No. 1.6e-25;  
 Matches 43; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 ETYGDWTAGVBAIRILQLFIHRIGCRHSRIGVTRQRARRGASRS 49  
 Db 48 DTYGDWTAGVBAIRILQLFIHRIGCRHSRIGVTRQRARRGASRS 96

Search completed: October 18, 2004, 18:52:23  
 Job time : 89.8125 secs



Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2004, 18:38:31 ; Search time 17.3542 Seconds  
(without alignments)  
271.671 Million cell updates/sec

Title: US-09-913-927D-3  
Perfect score: 254  
Sequence: 1 ETYGDWTAGVEAIIRLQQL.....RHSRIGVTRQRARRGASRS 49

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:  
1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	249	98.0	96	2 T09444	vpr protein - huma
2	244	96.1	96	2 S54380	vpr protein - huma
3	235	92.5	96	2 T01670	vpr protein - huma
4	233.5	91.9	95	2 T09383	vpr protein - huma
5	228	90.0	97	1 D44001	vpr protein - huma
6	205	80.7	95	1 ASLJSC	vpr protein - simi
7	120	47.2	89	1 S07991	vpr protein - simi
8	120	47.2	101	2 T11563	vpr protein - simi
9	120	47.2	105	2 S53095	vpr protein - huma
10	118	46.5	101	2 S08439	vpr protein - huma
11	117	46.1	122	1 ASLJRS	vpr protein - simi
12	116	45.7	105	1 ASLJR2	vpr protein - huma
13	115	45.3	101	1 ASLJR3	vpr protein - simi
14	113	44.5	104	1 ASLJCY	vpr protein - huma
15	111	43.7	97	2 S03067	gene R protein - huma
16	110.5	43.5	104	1 ASLJSY	vpr protein - huma
17	110	43.3	105	1 ASLJGR	vpr protein - huma
18	108	42.5	105	2 S12156	vpr protein - huma
19	67.5	26.6	119	1 ASLJX4	vpr protein - simi
20	56.5	22.2	314	2 C97332	ABC-type transport
21	55	21.9	178	2 T42535	hypothetical prote
22	54.5	21.5	328	2 H81996	probable integral
23	54.5	21.5	328	2 E81225	hypothetical prote
24	54	21.5	454	2 A13467	glycine betaine/1-
25	53.5	21.1	275	2 B55224	hypothetical prote
26	53	21.1	311	2 H53887	hypothetical prote
27	53	20.9	532	2 G84427	probable RNA-bind
28	52.5	20.7	341	2 F69171	2-oxoglutarate deh
29	51.5	20.3	282	2 C69553	ES5b protein - huma

## ALIGNMENTS

RESULT 1  
T09444  
vpr protein - human immunodeficiency virus type 1 (strain JRFL)  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 16-Jul-1999 #Sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T09444  
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, A;Accession number: Z16673  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-96 <PAN>  
A;Cross-references: UNIPROT:Q75757; EMBL:U63632; NID:91465777; PID:91465784  
C;Genetics:  
A;Gene: vpr  
C;Superfamily: AIDS vpr protein

Query Match 98.0%; Score 249; DB 2; Length 96;  
Best Local Similarity 95.9%; Pred. No. 7.6e-28;  
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQQLPFIHRTGCRHSIGVTRQRARRGASRS 49  
Db 48 ETYGDWTAGVEAIRILQQLPFIHRTGCRHSIGVTRQRARRGASRS 96

RESULT 2  
S54380  
vpr protein - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 15-Jul-1995 #Sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S54380  
R;Theodore, T.; Buckler-White, A.J.  
A;Accession number: S54377  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: RNA  
A;Residues: 1-96 <THE>  
A;Cross-references: UNIPROT:P12519; EMBL:M22639; NID:9329377; PID:AAA45368.1; PID:932936  
C;Superfamily: AIDS vpr protein

Query Match 96.1%; Score 244; DB 2; Length 96;  
Best Local Similarity 91.8%; Pred. No. 3.8e-27;  
Matches 45; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQQLPFIHRTGCRHSIGVTRQRARRGASRS 49  
Db 48 ETYGDWTAGVEAIRILQQLPFIHRTGCRHSIGVTRQRARRGASRS 96

RESULT 3  
T01670 vpr protein - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 09-Jul-2004  
R;Accession: T01670  
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.  
Cell 46, 63-74, 1986  
A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates  
A;Reference number: 214389; PMID:86245056; PMID:2424612  
A;Accession: T01670  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-96 <ALI>  
A;Cross-references: UNIPROT:PO5955; EMBL:K03456; NID:960228; PIDN:CAA28041.1; PID:960232  
C;Superfamily: AIDS vpr protein

Query Match 92.5%; Score 235; DB 2; Length 96;  
Best Local Similarity 89.8%; Pred. No. 7.2e-26;  
Matches 44; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRLQLLTHFRGCHSRIGTRQRARRGASRS 49  
Db 48 ETYGDWTAGVEAIRLQLLTHFRGCHSRIGTRQRARRGASRS 96

RESULT 4  
T09383 vpr protein - human immunodeficiency virus type 1 (isolate cntr1 1)  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Variety: isolate cntr1 1  
C;Accession: T09383  
R;Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Marianni, R.; Busch, M.P.; Bir  
J.; Virol. 69, 4228-4236, 1995  
A;Title: Defective accessory genes in a human immunodeficiency virus type 1-infected long-term culture  
A;Reference number: 216654; PMID:95287475; PMID:7769682  
A;Accession: T09383  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
A;Residues: 1-95 <ALI>  
A;Cross-references: UNIPROT:Q71925; EMBL:U24451; NID:g829440; PIDN:AAA79575.1; PID:98294  
C;Genetics:

Query Match 91.9%; Score 233.5; DB 2; Length 95;  
Best Local Similarity 93.9%; Pred. No. 1.2e-25;  
Matches 46; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 ETYGDWTAGVEAIRLQLLTHFRGCHSRIGTRQRARRGASRS 49  
Db 48 ETYGDWTAGVEAIRLQLLTHFRGCHSRIGTR-RRTRNGASRS 95

RESULT 5  
D44001 vpr protein - human immunodeficiency virus type 1 (strain YU-2)  
N;Alternative names: orf-R protein  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: D44001  
R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.  
J.; Virol. 66, 6581-6600, 1992  
A;Title: Complete nucleotide sequence, genome organization, and biological properties of the AIDS virus  
A;Reference number: A44001; MUID:93021387; PMID:1404605  
A;Accession: D44001  
A;Molecule type: DNA  
A;Residues: 1-97 <ALI>  
A;Cross-references: UNIPROT:P35967; GB:M93258  
C;Genetics:

Query Match 100.0%; Score 228.5; DB 1; Length 97;  
Best Local Similarity 90.0%; Pred. No. 6e-25;  
Matches 45; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 ETYGDWTAGVEAIRLQLLTHFRGCHSRIGTRORRARRGASRS 49  
Db 48 ETYGDWTAGVEAIRLQLLTHFRGCHSRIGTRORRARRGASRS 97

RESULT 6  
ASL-TSC vpr protein - simian immunodeficiency virus SIVcpz  
C;Species: simian immunodeficiency virus SIVcpz  
A;Note: host Pan troglodytes (Chimpanzee)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C;Accession: S09986  
R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.  
Nature 349, 356-359, 1990  
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.  
A;Reference number: S09983; MUID:90259077; PMID:2188136  
A;Accession: S09986  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-96 <HUE>  
A;Cross-references: UNIPROT:P12787; EMBL:X52154; PIDN:CAA36403.1; PID:958866; PIDN:CAA36403.1; PID:958870  
C;Genetics:

Query Match 80.7%; Score 205; DB 1; Length 96;  
Best Local Similarity 75.5%; Pred. No. 1.3e-21;  
Matches 37; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRLQLLTHFRGCHSRIGTRORRARRGASRS 49  
Db 48 DRYGDWTAGVEAIRLQLLTHFRGCHSRIGTRORRARRGASRS 96

RESULT 7  
S07991 vpr protein - simian immunodeficiency virus SIVsm (isolate F236)  
C;Species: simian immunodeficiency virus SIVsm  
A;Note: host Cercocebus torquatus atys (sooty mangabey)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: S07991  
R;Hirsch, V.M.; Olmsted, R.A.; Murphey-Corb, M.; Purcell, R.H.; Johnson, P.R.  
Nature 339, 386-392, 1989  
A;Title: An African primate lentivirus (SIV(sm)) closely related to HIV-2.  
A;Reference number: S04237; MUID:89262053; PMID:2786147  
A;Accession: S07991  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: genomic RNA  
A;Residues: 1-89 <HUE>  
A;Cross-references: UNIPROT:P12521; EMBL:X14307; NID:961741; PIDN:CAA32486.1; PID:961745  
C;Genetics:  
A;Note: this sequence was submitted to the EMBL Data Library, February 1989  
A;Gene: vpr  
C;Superfamily: AIDS vpr protein

Query Match 47.2%; Score 120; DB 2; Length 89;  
Best Local Similarity 60.5%; Pred. No. 1.2e-09;  
Matches 23; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRLQLLTHFRGCHSRIGTRORRARRGASRS 38  
Db 49 DRHGDPLEGAGELIRLQLRPLFHRSGCAHSRIGGSR 86

RESULT 8						
T11563	vpr protein - simian immunodeficiency virus SIV <sub>m</sub> (strain B543)					
C;Species: simian immunodeficiency virus SIV <sub>m</sub>						
A;Variety: strain B543						
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004						
C;Accession: T11563						
R.Hirsch, V.M.; Adter-Johnson, D.; Campbell, B.; Goldstein, S.; Brown, C.; Elkins, W.R.; J. Virol. 71, 1608-1620, 1997						
A;Title: A molecularly cloned, pathogenic, neutralization-resistant simian immunodeficiency virus number 217285; MUID:9715152; PMID:8995688						
A;Accession: T11563						
A;Status: preliminary; translated from GB/EMBL/DBJU						
A;Molecule type: DNA						
A;Residues: 1-101 <HIV>						
A;Cross-references: UNIPROT: D89157; EMBL: U72748; NID: 91695908; PIDN: AAC56562.1; PID: 9169						
C;Genetics:						
A;Gene: vpr						
C;Superfamily: AIDS vpr protein						
C;Keywords: AIDS; immunodeficiency						
Query Match Score 120; DB 2; Length 101;						
Best Local Similarity 60.5%; Pred. No. 1.4e-09;						
Matches 23; Conservative 5; Mismatches 10; Indels 0; Gaps 0;						
Qy 1 EYGTDTWAGVEAIIRLQQLIFTHFRIGCRHSRIGVTR 38						
Db 49 DRHGTLEGAGELIRLQLRAPHFRSGCAHSRIGOSR 86						
RESULT 9						
S53095	vpr protein - human immunodeficiency virus type 2					
C;Species: human immunodeficiency virus type 2, HIV-2						
C;Accession: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004						
R.J.Becker, M.; Zorr, B.; Becker, A.; Habermehl, K.O.						
submitted to the EMBL Data Library, March 1995						
A;Description: Molecular and phylogenetic characterisation of a Guinea-Bissau-derived human immunodeficiency virus						
A;Accession: S53095						
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-105 <HIV>						
A;Cross-references: UNIPROT: Q76624; EMBL: Z48731; NID: 9732718; PIDN: CAA88624.1; PID: 97327						
C;Superfamily: AIDS vpr protein						
Query Match Score 120; DB 2; Length 105;						
Best Local Similarity 63.9%; Pred. No. 1.4e-09;						
Matches 23; Conservative 3; Mismatches 10; Indels 0; Gaps 0;						
Qy 3 YGDTWAGVEAIIRLQQLIFTHFRIGCRHSRIGVTR 38						
Db 55 HGDTLEGAGELIRLQLRAPHFRSGCAHSRIGQTR 90						
RESULT 10						
S08439	vpr protein - human immunodeficiency virus type 2, D205					
C;Species: human immunodeficiency virus type 2 D205, HIV-2 D205						
C;Accession: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004						
R.J.Dietrich, U.; Adamski, M.; Kreutz, R.; Seipp, A.; Ruebsamen-Waigmann, H.						
Nature 342, 948-950, 1989						
A;Title: A highly divergent HIV-2-related isolate.						
A;Reference number: S08439						
A;Accession: S08439						
A;Status: nucleic acid sequence not shown; translation not shown						
A;Molecule type: DNA						
A;Residues: 1-101 <HIV>						
A;Cross-references: UNIPROT: P15937; EMBL: X16109						
A;Note: this sequence was submitted to the EMBL Data Library, Aug-1999						

vpr protein - simian immunodeficiency virus (macaque isolate)

C; Alternate names: orf-R protein  
C; Species: simian immunodeficiency virus, SIV

C; Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 16-Jul-1999  
C; Accession: E28887

R; Chakrabarti, L.; Guyader, M.; Alizon, M.; Daniell, M.D.; Desrosiers, R.C.; Tiollais, P.  
Na; Nature 28, 543-547, 1987

A; Title: Sequence of simian immunodeficiency virus from macaque and its relationship to  
A; Reference number: A28887; MUID:87287230; PMID:3649576

A; Accession: E28887

A; Molecule type: DNA

A; Residues: 1-101 <CHA>

A; Cross-references: GB:Y00277; GB:M16403; NID:961730; PID:CAA68383.1; PID:961735

C; Genetics:

A; Gene: vpr  
C; Superfamily: AIDS vpr protein

C; Keywords: AIDS; immunodeficiency

Query Match 45.3%; Score 115; DB 1; Length 101;

Best Local Similarity 66.7%; Pred. No. 7e-09;  
Matches 22; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 3 YGDTWAGVEAIRLQLLFIHFRIGCRHSRIG 35  
Db 51 HGDITLEGAEILIRLQLRALFIHRSGCNSRIG 83

RESULT 14

AS Lucy  
vpr protein - human immunodeficiency virus type 2 (isolate CAM2/Guinea-Bissau)

N; Alternate names: orf-R protein  
C; Species: human immunodeficiency virus type 2, HIV-2

A; Note: host Homo sapiens (man)

C; Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C; Accession: E38475; J00977

R; Tristem, M.; Hill, F.; Karpas, A.

J. Gen. Virol. 72, 721-724, 1991

A; Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus type

A; Reference number: A31475; MUID:91170959; PMID:2005437

A; Accession: E38475

A; Molecule type: DNA

A; Residues: 1-104 <TRI>

A; Cross-references: UNIPROT:P24111; GB:D00835; NID:93153166; PIDN:BAA00713.1; PID:922147

C; Genetics:

A; Gene: vpr  
C; Superfamily: AIDS vpr protein

C; Keywords: AIDS; immunodeficiency

Query Match 44.5%; Score 113; DB 1; Length 104;

Best Local Similarity 58.3%; Pred. No. 1.4e-08;  
Matches 21; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 3 YGDTWAGVEAIRLQLLFIHFRIGCRHSRIG 38  
Db 55 HGDITLEGAEILIRLQLRALFIHRSGCNSRIG 90

RESULT 15

S03067  
Gene R protein - human T-cell lymphotropic virus type 4

C; Species: human T-cell lymphotropic virus type 4, HTLV-4

C; Date: 21-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C; Accession: S03067

R; Hahn, B.H.; Kong, L.I.; Lee, S.W.; Kumar, P.; Taylor, M.P.; Arya, S.K.; Shaw, G.M.

Nature 300, 184-186, 1987

A; Title: Relation of HTLV-4 to simian and human immunodeficiency-associated viruses.

A; Reference number: S03065

A; Accession: S03067

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-97 <TAH>

A; Cross-references: UNIPROT:Q85605; EMBL:X06391; NID:961580; PID:CAA29689.1; PID:961582

A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1987

C; Superfamily: AIDS vpr protein

Query Match 43.7%; Score 111; DB 2; Length 97;  
Best Local Similarity 63.6%; Pred. No. 2.5e-08;  
Matches 21; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 3 YGDTWAGVEAIRLQLLFIHFRIGCRHSRIG 35  
Db 51 HGDITLEGAEILIRLQLRALFIHRSGCNSRIG 83

Search completed: October 18, 2004, 18:48:21  
Job time : 18.3542 secs

Scoring table: BLOSUM62								Alignments											
Gapop 10.0 , Gapext 0.5																			
Searched: 1825181 seqs, 575374646 residues																			
Total number of hits satisfying chosen parameters: 1825181																			
Minimum DB seq length: 0								RESULT 1											
Maximum DB seq length: 2000000000								ID = VPR_HV1NS	STANDARD;	PRT;	96 AA.	VPR_HV1NS							
Post-processing: Minimum Match 0%								AC P12520;				Q9iqb1							
Maximum Match 100%								DT 01-OCT-1989	(Rel. 12, Created)			Q9ic6							
Listing first 45 summaries								DT 01-FEB-1996	(Rel. 33, Last sequence update)			Q900a1							
Database : UniProt_02:*								DT 01-OCT-2004	(Rel. 45, Last annotation update)			Q90288							
1: uniprot_sprot:*								DB VPR Protein (R ORF Protein).				Aar24626							
2: uniprot_trembl:*								GN Name=VPR;				Aar24629							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.								CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).										
SUMMARIES								CC	EMBL: M19921; AAA44990.1; -.										
Result No.	Score		Query		Match		Length		DB	ID	DR	PDB; 1BDB; NMR; Q=49-53.	Q9iqb1						
1	254	100.0	96	1	VPR_HV1NS		P12220	human	immun	P20983	DR	PDB; 1DSJ; NMR; Q=49-53.	Q9ic6						
2	253	99.6	96	1	VPR_HV1JR		P68203	human	immun	Q68203	DR	PDB; 1DSK; NMR; Q=59-86.	Q900a1						
3	253	99.6	96	2	Q6SZU3		Q9iob7	human	immun	Aar24628	DR	PDB; 1K2S; NMR; A=33-57.	Q90288						
4	253	99.6	96	2	Q6SZU3		Aar24628	human	immun	071267	DR	PDB; 1K2T; NMR; A=33-52.	Aar24629						
5	253	99.6	96	2	AAR24628		090307	human	immun	Q6q940	DR	PDB; 1K2V; NMR; A=33-52.	Q90288						
6	252	99.2	96	2	071267		Q6q940	human	immun	Aab86190	DR	DR; M19921; VPRSNL43.	Q9iob7						
7	252	99.2	96	2	071267		Aab86190	human	immun	P05228	DR	DR; InterPro; IPR00012; Retrov_VPR/X.	Q9iob8						
8	251	98.8	96	2	Q6q940		P05228	human	immun	P05228	DR	Pfam; PF00522; VPR; 1.	P05254						
9	251	98.8	96	2	AAS86190		P05228	human	immun	P05228	DR	PRINTS; PR00044; HIVVPRPX.	O36203						
10	250	98.4	96	1	VPR_HV1BR		P05228	human	immun	Q68203	FT HELIX	3D-structure, AIDS, 52	O6J173						
11	250	98.4	96	1	Q9iob8		P05228	human	immun	Q78029	FT HELIX	52	Q68203						
12	249	98.0	96	1	VPR_HV1RH		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
13	249	98.0	96	2	Q66203		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
14	249	98.0	96	2	Q6J173		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
15	249	98.0	96	2	Q68203		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
16	249	98.0	96	2	Q68203		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
17	249	98.0	96	2	Q71299		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
18	249	98.0	96	2	Q72014		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
19	249	98.0	96	2	Q75757		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
20	249	98.0	96	2	Q79234		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
21	249	98.0	96	2	Q79245		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
22	249	98.0	96	2	Q9iQAS		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
23	249	98.0	96	2	Q78029		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
24	249	98.0	96	2	Q78042		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
25	249	98.0	96	2	Q6H1N6		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
26	249	98.0	96	2	Q720J96		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
27	249	98.0	96	2	Q9iQAS		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
28	249	98.0	96	2	Q9iQAS		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
29	249	98.0	96	2	Q9iQAS		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
30	249	98.0	96	2	Q9iQAS		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
31	249	98.0	96	2	Q9iQAS		P05228	human	immun	Q78029	SEQUENCE	96 AA; 11379 MW; 58BC53573479D150 CRC64;	Q78029						
RESULT 2								QY	1	ETIGDTWAGVEAIRLQLFHRIGCRHSIGVTQRRANGASRS	49	Q9iQAS							
ID = VPR_HV1JR								DB	48	ETIGDTWAGVEAIRLQLFHRIGCRHSIGVTQRRANGASRS	96	Q9iQAS							
AC P27883;								DT	01-FEB-1991	(Rel. 17, Created)		Q9iQAS							

DT	01-FEB-1991 (Rel. 17, Last sequence update)	RESULT 4
DT	01-OCT-2004 (Rel. 45, Last annotation update)	Q91BN7 PRELIMINARY; PRT; 96 AA.
DE	VPR protein (R ORF protein).	AC Q91BN7; PRELIMINARY; PRT;
GN	Name=vpr;	AC Q91BN7;
OS	Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).	AC Q91BN7; PRELIMINARY; PRT;
OC	Viruses; Retroviridae; Lentiviridae; Lentivirus.	AC Q91BN7; PRELIMINARY; PRT;
OX	NCBI_TaxID:11688;	DT 01-OCT-2000 (TREMBLrel. 15, Created)
RN	[1]	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
RP	SEQUENCE FROM N.A.	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
RA	Keyangsi S., Chen I. S.Y.;	DB VPR protein.
RL	Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.	DB NCBITaxID:11676;
CC		OS Human immunodeficiency virus 1.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	OC Viruses; Retroviridae; Lentiviridae; Lentivirus.
CC		OX
CC		RN [1] _
CC		RN Sequence FROM N.A.
CC		RP STRAIN=subtype B;
CC		RC MEDLINE=96100012; PubMed=7483788;
CC		RX Vella C., Smith M.H., Farrar G.H., Jones D.H., Daniels R.S.; Daniels R.S.; Greenaway P.J.;
CC		RT "A molecular and serologic study of the envelope gene of the British isolate: HIV-1 GB8.";
CC		RT isolate: HIV-1 GB8.;"
CC		RT Vaccine 13:735-741 (1995).
DR	M38429; AAB03747.1; -.	RL [2]
DR	HSSP; P122520; 1BDE.	RN RN
DR	HIV; M38429; VPR\$JRCSF.	RC SEQUENCE FROM N.A.
DR	InterPro; IPR000012; Retrov_VPR/X.	RC STRAIN=subtype B;
DR	Pfam; PF00522; VPR; 1.	RC MEDLINE=9136614; PubMed=1890410;
DR	PRINTS; PR00444; HIVVPRVX.	RA Farrar G.H., Roff M.A., Amin T., Ball J., Garrett A.M.,
RW	AIDS. SEQUENCE 96 AA; 11419 MW;	RA Baracharya U., Booth J., Wansbrough-Jones M.H., Greenaway P.J.,
RW	069545878BED2925 CRC64;	RA RT "Characterisation of a series of human immunodeficiency virus isolates derived sequentially from a single patient.";
RW	Score 99.6%; Score 253; DB 1; Length 96;	RT J. Med. Virol. 34:104-113 (1991).
QM	Best Local Similarity 98.0%; Pred. No. 1e-26;	RL RN
QM	Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	RP Sequence FROM N.A.
QM	1 ETYGDWTAGVEAATRILQLQLFTHFRIGCRHSRIGTRQRARRGASRS 49	RC STRAIN=subtype B;
Db	48 ETYGDWTAGVEAATRILQLQLFTHFRIGCRHSRIGTRQRARRGASRS 96	RC MEDLINE=20416339; PubMed=10954893;
QM	Score 99.6%; Score 253; DB 1; Length 96;	RA Novelli P., Vella C., Oxford J.S., Daniels R.S.; Daniels R.S.;
Db	Best Local Similarity 98.0%; Pred. No. 1e-26;	RT RT "Biological characterisation of an infectious molecular clone of HIV Type 1GB8.";
QM	Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	RT AIDS Res. Hum. Retroviruses 16:1175-1178 (2000).
QM	1 ETYGDWTAGVEAATRILQLQLFTHFRIGCRHSRIGTRQRARRGASRS 49	DR DR EMBL; AJ271445; CAB92789.1; -.
Db	48 ETYGDWTAGVEAATRILQLQLFTHFRIGCRHSRIGTRQRARRGASRS 96	DR DR HSSP; P12520; 1BDE.
QM	Score 99.6%; Score 253; DB 2; Length 96;	DR DR InterPro; IPR000012; Retrov_VPR/X.
Db	Best Local Similarity 98.0%; Pred. No. 1e-26;	DR DR Pfam; PF00522; VPR; 1.
GN	Name=vpr;	KW AIDS
GN	Human immunodeficiency virus 1.	FT CHAIN 1 20 vif.
OS	Viruses; Retroviridae; Lentiviridae; Lentivirus.	FT CHAIN 1 96 vpr.
OX	NCBI_TaxID:11676;	FT CHAIN 1 96 tat.
RP	SEQUENCE FROM N.A.	FT SEQUENCE 96 AA; 11293 MW; C0005A439E0DD92E CRC64;
DR	PubMED=15166526;	Query Match 99.6%; Best Local Similarity 98.0%; Score 253; DB 2; Length 96;
DR	InterPro; IPR000012; Retrov_VPR/X.	Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	Pfam; PF00522; VPR; 1.	DR Vpr protein.
DR	PRINTS; PR00444; HIVVPRVX.	AC AAR24628; PRELIMINARY; PRT; 96 AA.
RW	SEQUENCE 96 AA; 11353 MW;	AC AAR24628; PRELIMINARY; PRT; 96 AA.
RW	9576F4AFEDB1244 CRC64;	AC AAR24628; PRELIMINARY; PRT; 96 AA.
DR	ENBL; AY44421; AAR24628.1;	AC AAR24628; PRELIMINARY; PRT; 96 AA.
DR	InterPro; IPR000012; Retrov_VPR/X.	AC AAR24628; PRELIMINARY; PRT; 96 AA.
DR	Pfam; PF00522; VPR; 1.	DT 02-MAR-2004 (TREMBLrel. 27, Created)
DR	PRINTS; PR00444; HIVVPRVX.	DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
RW	SEQUENCE 96 AA; 11353 MW;	DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
RW	9576F4AFEDB1244 CRC64;	DE Vpr protein.
DR	Score 99.6%; Score 253; DB 2; Length 96;	GN Human immunodeficiency virus 1.
DR	Best Local Similarity 98.0%; Pred. No. 1e-26;	OS Viruses; Retroviridae; Lentiviridae; Lentivirus.
DR	Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	OC Primate Lentivirus group.
QM	1 ETYGDWTAGVEAATRILQLQLFTHFRIGCRHSRIGTRQRARRGASRS 49	OC NCBITaxID:11676;
Db	48 ETYGDWTAGVEAATRILQLQLFTHFRIGCRHSRIGTRQRARRGASRS 96	OX RN
QM	Score 99.6%; Score 253; DB 2; Length 96;	RP Sequence FROM N.A.
Db	Best Local Similarity 98.0%; Pred. No. 1e-26;	RC STRAIN=9;



Qy	1	ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 49	OX	NCBI_TaxID=11676;
Db	48	ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 96	RN	SEQUENCE FROM N.A.
			RP	SEQUENCE FROM N.A. PubMed=10881687;
			RX	Medline=20338556; PubMed=10881687;
			RA	Yamada T.; Iwamoto A.;
			RT	"Comparison of proviral accessory genes between long-term nonprogressors and progressors of human immunodeficiency virus type 1 infection." Arch. Virol. 145:1021-1027 (2000).
			RL	EMBL; AB034527; BAA93974.1; -.
			DR	HSSP; P12520; 1BDE.
			DR	Integro; IPR00012; Retrov_VpR/X.
			DR	Pfam; PF00522; VPR; 1.
			DR	PRINTS; PR00444; HIVVPRVX.
			KW	AIDS.
			SQ	SEQUENCE 96 AA; 11365 MW; 9EAAFP998E0B6DD80 CRC64;
				Query Match 98.4%; Score 250; DB 1; Length 96;
				Best Local Similarity 95.3%; Pred. No. 2.6e-26;
				Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy	1	ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 49	Qy	1 ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 49
Db	48	ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 96	Db	48 ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 96
				SEQUENCE FROM N.A.
			RP	VPR_HV1RH STANDARD PRT; 96 AA.
			ID	VPR_HV1RH ID P05934;
			AC	AC P05934; 01-NOV-1988 (Rel. 09, Created)
			DT	DT 01-NOV-1988 (Rel. 09, Last sequence update)
			CC	CC 01-OCT-2004 (Rel. 45, Last annotation update)
			DT	DT 01-OCT-2004 (Rel. 45, Last annotation update)
			DB	DB VPR Protein (R ORF protein).
			GN	GN Name=VPR;
			OS	OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
			OC	OC Viruses; Retroviridae; Lentiviridae; Lentivirus.
			OX	OX NCBI_TaxID=11686;
			RN	RN [1]
			RP	SEQUENCE FROM N.A. (CLONE PN4-3).
			RA	RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
			RL	RL Submitted (TUN-1988) to the EMBL/GenBank/DBJ databases.
			CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. There are no restrictions on its use by commercial entities. This statement is not removed, usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
			CC	CC EMBL; K02013; AAB59749.1; -.
			DR	DR HSSP; P12520; 1BDE.
			DR	DR HIV; K02013; VPRBRU.
			DR	DR HIV; M1921; VPRNL43.
			DR	DR Integro; IPR00012; Retrov_VpR/X.
			DR	DR Pfam; PF00522; VPR; 1.
			DR	DR PRINTS; PR00444; HIVVPRVX.
			AIDS	AIDS.
			FT	FT CONFLICT 15 15 H -> Y (in Ref. 2).
			FT	FT CONFLICT 28 28 N -> S (in Ref. 2).
			FT	FT CONFLICT 41 41 G -> N (in Ref. 2).
			FT	FT CONFLICT 85 85 Q -> R (in Ref. 2).
			FT	FT CONFLICT 85 85 42892A4186B3D3E CRC44;
			SQ	SQ SEQUENCE 96 AA; 11295 MW; 42892A4186B3D3E CRC44;
				Query Match 98.4%; Score 250; DB 1; Length 96;
				Best Local Similarity 98.0%; Pred. No. 2.6e-26;
				Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1	ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 49	Qy	1 ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 49
Db	48	ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 96	Db	48 ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 96
				SEQUENCE 96 AA; 11338 MW; 85BC4E4D5CF17741 CRC64;
			CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
			CC	CC EMBL; M17451; AAA45055.1; -.
			CC	CC DR PDB; 1F10; NMRA_A=12-33.
			CC	CC DR HIV; M17451; VPRSRF.
			CC	CC DR Integro; IPR00012; Retrov_VpR/X.
			CC	CC DR Pfam; PF00522; VPR; 1.
			CC	CC DR PRINTS; PR00444; HIVVPRVX.
			KW	KW 3D-structure; AIDS.
			SQ	SQ SEQUENCE 96 AA; 11338 MW; 85BC4E4D5CF17741 CRC64;
				Query Match 98.0%; Score 249; DB 1; Length 96;
				Best Local Similarity 95.3%; Pred. No. 3.6e-26;
				Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy	1	ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 49	Qy	1 ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 49
Db	48	ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 96	Db	48 ETYGDWTWAGVEAIRLQLLFIHFRGCRHSRIGVTRQRARRGASRS 96
				SEQUENCE 96 AA; 11338 MW; 85BC4E4D5CF17741 CRC64;
			CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
			CC	CC EMBL; M17451; AAA45055.1; -.
			CC	CC DR PDB; 1F10; NMRA_A=12-33.
			CC	CC DR HIV; M17451; VPRSRF.
			CC	CC DR Integro; IPR00012; Retrov_VpR/X.
			CC	CC DR Pfam; PF00522; VPR; 1.
			CC	CC DR PRINTS; PR00444; HIVVPRVX.
			KW	KW 3D-structure; AIDS.
			SQ	SQ SEQUENCE 96 AA; 11338 MW; 85BC4E4D5CF17741 CRC64;
				Query Match 98.0%; Score 249; DB 1; Length 96;
				Best Local Similarity 95.3%; Pred. No. 3.6e-26;
				Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Q9IQB8		PRELIMINARY	PRT;	96 AA.
ID	Q9IQB8			AC Q9IQB8; 15, Created)
AC	Q9IQB8			DT 01-OCT-2000 (TREMBLrel. 15,
DT	Q9IQB8			DT 01-OCT-2000 (TREMBLrel. 15,
DT	Q9IQB8			DT 01-JUN-2003 (TREMBLrel. 24,
DT	Q9IQB8			DE Vpr protein.
GN	Q9IQB8			GN Name=vpr;
OS	Q9IQB8			OS Human immunodeficiency virus 1.
OC	Q9IQB8			OC Viruses; Retroviridae; Lentivirus.

RESULT 13

Q6SZU2 PRELIMINARY; PRT; 96 AA.

Q6SZU2; PRELIMINARY; PRT; 96 AA.

AC 036203; PRELIMINARY; PRT; 96 AA.

AC 036203; PRELIMINARY; PRT; 96 AA.

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Vpr protein.

GN Name=vpr;

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

NCBI\_TaxID=11676;

OX RN [1]

RP SEQUENCE FROM N.A.

RA Sakaena N.; Wang B.; Ge Y.C.; Dwyer D.; Downton D.; Cunningham A., Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF000315; AB070154.1; -.

DR HSSP; P12820; 1DSJ.

DR InterPro; IPR00012; RetroV\_VPR/X.

DR Pfam; PF00522; VPR; 1.

DR AIDS.

KW AIDS.

SQ SEQUENCE 96 AA; 11349 MW; 06954E5151109B4C CRC64;

Query Match 98.0%; Score 249; DB 2; Length 96;

Best Local Similarity 95.9%; Pred. No. 3.6e-26;

Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQLQFLIHRIGCHSRIGVTRQRARGASRS 49

Db 48 ETYGDWTAGVEAIRILQLQFLIHRIGCHSRIGVTRQRARGASRS 96

Q6JN73 PRELIMINARY; PRT; 96 AA.

Q6JN73; PRELIMINARY; PRT; 96 AA.

AC 06JN73; PRELIMINARY; PRT; 96 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Vpr protein.

GN Name=vpr;

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

NCBI\_TaxID=11676;

OX RN [1]

RP SEQUENCE FROM N.A.

RA Tovanabutra S.; Beyer C.; Sakkachornphop S.; Razak M.H.; Ramos G.I., Vongchak T.; Rungruengthanaikit K.; Saethioe P.; TejaCong K.; Kim B., De Souza M.; Robb M.L.; Birx D.L.; Jittiwutikarn J.; Suriyanon V., Celentano D.D.; McCutchan F.E., "The Changing Molecular Epidemiology of HIV Type 1 among Northern Thai Drug Users, 1999 to 2002." AIDS Res Hum Retroviruses 20:465-475 (2004).

RL InterPro; IPR00012; RetroV\_VPR/X.

DR Pfam; PF00522; VPR; 1.

DR AIDS.

SQ SEQUENCE 96 AA; 11205 MW; 9B009C38EBB30B7EE CRC64;

Query Match 98.0%; Score 249; DB 2; Length 96;

Best Local Similarity 95.9%; Pred. No. 3.6e-26;

Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQLQFLIHRIGCHSRIGVTRQRARGASRS 49

Db 48 ETYGDWTAGVEAIRILQLQFLIHRIGCHSRIGVTRQRARGASRS 96

RESULT 14

Q6JN73 PRELIMINARY; PRT; 96 AA.

Q6JN73; PRELIMINARY; PRT; 96 AA.

AC 06JN73; PRELIMINARY; PRT; 96 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Vpr protein.

GN Name=vpr;

OS Human immunodeficiency virus 1.

OC Viruses; Retroviridae; Lentivirus.

NCBI\_TaxID=11676;

OX RN [1]

RP SEQUENCE FROM N.A.

RA Tovanabutra S.; Beyer C.; Sakkachornphop S.; Razak M.H.; Ramos G.I., Vongchak T.; Rungruengthanaikit K.; Saethioe P.; TejaCong K.; Kim B., De Souza M.; Robb M.L.; Birx D.L.; Jittiwutikarn J.; Suriyanon V., Celentano D.D.; McCutchan F.E., "The Changing Molecular Epidemiology of HIV Type 1 among Northern Thai Drug Users, 1999 to 2002." AIDS Res Hum Retroviruses 20:465-475 (2004).

RL InterPro; IPR00012; RetroV\_VPR/X.

DR Pfam; PF00522; VPR; 1.

DR AIDS.

SQ SEQUENCE 96 AA; 11205 MW; 9B009C38EBB30B7EE CRC64;

Query Match 98.0%; Score 249; DB 2; Length 96;

Best Local Similarity 95.9%; Pred. No. 3.6e-26;

Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ETYGDWTAGVEAIRILQLQFLIHRIGCHSRIGVTRQRARGASRS 49

Db 48 ETYGDWTAGVEAIRILQLQFLIHRIGCHSRIGVTRQRARGASRS 96

RESULT 15

THIS PAGE BLANK (uspto)